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OM protein - protein search, using sw model

Run on: October 21, 2004, 11:48:04 ; Search time 155 Seconds

(without alignments)
1053.044 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385
Sequence: 1 MSFYSQDYNMDELEBYN.....GFLNGIKADLVSLIHLHM 455

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04.*
1: geneseq1980s.*
2: geneseq1990s.*
3: geneseq2000s.*
4: geneseq2001s.*
5: geneseq2002s.*
6: geneseq2003as.*
7: geneseq2003bs.*
8: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2385	100.0	455	2	AAR95939 Human Y5
2	2385	100.0	455	2	AAW29447 Human hip
3	2385	100.0	455	2	AAW29413 Human hip
4	2385	100.0	455	2	AAW37093 Homo sapi
5	2385	100.0	455	2	AAW57461 Human hip
6	2385	100.0	455	4	AAE08002 Human neu
7	2385	100.0	455	5	ABE84497 Human hip
8	2385	100.0	455	5	ABE79510 Human neu
9	2385	100.0	455	8	AAO23266 Human neu
10	2385	100.0	455	8	ADO29564 Human GPC
11	2373	99.5	445	4	AAE08016 African g
12	2330	97.7	445	2	AAW27604 Human neu
13	2330	97.7	445	2	AAW15230 Human neu
14	2330	97.7	445	2	AAW14554 Human neu
15	2330	97.7	445	3	AAW52578 Human NPY
16	2330	97.7	445	4	AAE07958 Human neu
17	2330	97.7	445	4	AAE06692 Human neu
18	2330	97.7	445	4	AAE07922 Human neu
19	2330	97.7	445	4	AAE85121 Human neu
20	2330	97.7	445	4	AAE85110 Human neu
21	2330	97.7	445	6	ABP81860 Cancer/an
22	2330	97.7	445	7	Adn39350 Human chi
23	2326	97.5	439	4	AAE08004 Human chi
24	2326	97.5	439	5	ABG32254 Neuropt
25	2321	97.3	445	4	ABE56370 Non-endog

26	2318	97.2	445	4	AAE02851 Rhesus ne
27	2266	95.0	445	3	AAW52577 Chimeric
28	2262	94.8	456	2	AAW37095 Canis dom
29	2084.5	87.4	456	2	AAW5940 Rat Y5 re
30	2084.5	87.4	456	2	AAW29446 Rat hypot
31	2084.5	87.4	456	2	AAW29412 Rat hypot
32	2084.5	87.4	456	2	AAW37092 Rattus no
33	2084.5	87.4	456	2	AAW57460 Rat hypot
34	2084.5	87.4	456	5	ABB84496 Rat hypot
35	2074.5	87.0	445	2	AAW27603 Rat neuro
36	2074.5	87.0	445	2	AAW14553 Rat neuro
37	2074.5	87.0	445	3	AAW52579 Rat NPY (
38	2074	87.0	445	3	AAW15233 Mouse neu
39	2072.5	86.9	445	2	AAW15232 Rat neuro
40	2070	86.8	466	8	ADO29565 Mouse GPC
41	2067.5	86.7	445	2	AAW27602 Rat neuro
42	2067.5	86.7	445	2	AAW14552 Rat neuro
43	2030.5	85.1	499	4	AAE08012 Rat chine
44	2017	84.6	508	4	AAE08010 Mouse chi
45	1671	70.1	334	2	AAW5941 Canine Y5

ALIGNMENTS

RESULT 1

AAW5939
ID AAR95939 standard; protein; 455 AA.

XX AAR95939;

XX 14-OCT-1996 (first entry)

XX Human Y5 receptor.

XX Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior;

KW G protein-coupled receptor; agonist; antagonist; obesity; bulimia;

KW anorexia; transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 51..77

FT /label= I

FT /note= "transmembrane domain I"

FT Domain 88..110

FT /label= II

FT /note= "transmembrane domain II"

FT Domain 126..147

FT /label= III

FT /note= "transmembrane domain III"

FT Domain 166..187

FT /label= IV

FT /note= "transmembrane domain IV"

FT Domain 220..242

FT /label= V

FT /note= "transmembrane domain V"

FT Domain 380..403

FT /label= VI

FT /note= "transmembrane domain VI"

FT Domain 416..438

FT /label= VII

FT /note= "transmembrane domain VII"

XX WO9616542-A1.

XX 06-JUN-1996.

XX 01-DEC-1995; 95WO-US015646.

XX 02-DEC-1994; 94US-00349025.

XX (SYNA-) SYNAPTIC PHARM CORP.

PA

XX Gerald CPG, Walker MW, Branchek T, Weinshank RL;
 XX WPI: 1996-277371/28.
 DR N-PSDB; AAT30433.
 XX Modifying feeding behaviour using Y5 receptor (ant)agonists - increases
 PT or decreases food consumption, for treatment of e.g. obesity or bulimia.
 XX Claim 51; Fig 6; 235pp; English.
 XX Human hippocampal Y5 receptor (AAR95939) was identified as the homologue
 CC of rat hypothalamic Y5 receptor (AAR95940), isolated as an 'atypical Y1
 CC receptor'. The receptor belongs to the G protein-coupled receptor
 CC superfamily. It is encoded by a cDNA clone (see also AAT30433) that was
 CC isolated from a hippocampus cDNA library using rat Y5 receptor cDNA as
 CC probe. Recombinant rat Y5 receptor can be produced in prokaryotic or
 CC eukaryotic (e.g. COS, 293 or Sf9 insect) host cells. It is used to
 CC identify Y5 ligands (agonists and antagonists) that can be used to treat
 CC obesity, bulimia or anorexia, and to raise monoclonal antibodies useful
 CC in detecting Y5 receptor
 XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-236; Indels 0; Gaps 0;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFYSKQDYNMDELEDEYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60
 DB 1 MSFYSKQDYNMDELEDEYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60
 QY 61 VSLGFMGNLLILMALMKRKNQKTTNVLGNLAFSDILVLFCSPPFLTSLVLDQWFG 120
 DB 61 VSLGFMGNLLILMALMKRKNQKTTNVLGNLAFSDILVLFCSPPFLTSLVLDQWFG 120
 QY 121 KVMCHIMPLOCVSVLVSTLILISAIIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
 DB 121 KVMCHIMPLOCVSVLVSTLILISAIIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240
 DB 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240
 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLPHVTTDFDNDNLISNRHFKLVYCIC 420
 DB 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLPHVTTDFDNDNLISNRHFKLVYCIC 420
 QY 421 HLLGMWSCCLPILYGLFNGGIKADLVSLIHCLHM 455
 DB 421 HLLGMWSCCLPILYGLFNGGIKADLVSLIHCLHM 455

RESULT 2
 AAW29447
 ID AAW29447 standard; protein; 455 AA.
 XX AAW29447;
 XX AAW29447;
 DT 25-MAR-2003 (revised)
 DT 26-FEB-1998 (first entry)
 DE Human hippocampal neuropeptide Y Y5 receptor.
 XX Hippocampal; neuropeptide Y Y5 receptor; NPV Y5; antagonist;

KW epileptic seizure; migraine; sleep disturbance; prophylaxis;
 KW eating disorder; quinazolin-2,4-diazirine.
 XX Homo sapiens.
 OS W09720822-A1.
 XX 12-JUN-1997.
 XX 18-NOV-1996; 96WO-EP005066.
 XX 01-DEC-1995; 95US-00566027.
 XX (NOVS) NOVARTIS AG.
 XX Rueeger H, Schmidlin T, Rigollier P, Yamaguchi Y,
 PI Tintelnotblomley M, Schilling W, Criscione L;
 PI NPI; 1997-319712/29.
 XX N-PSDB; AAT89114.
 XX Use of new and known quinazolin-2,4-diazirine compounds as NPV Y5
 PT receptor antagonists - for treating and preventing eating disorders,
 PT diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
 PT migraine, sleep disturbance, etc.
 XX Disclosure; Page 127-129; 155pp; English.
 XX The present sequence represents human hippocampal neuropeptide (NP) Y
 CC receptor subtype Y5, with a pharmacological function associated with for
 CC example, obesity and eating disorders. The specification relates to a
 CC method of treatment and prophylaxis of disorders and diseases associated
 CC with with NP receptor subtype Y5 comprising administering to a warm-
 CC blooded animal, including man, in need of such treatment a
 CC therapeutically effective amount of a quinazolin-2,4-diazirine compound.
 CC These disorders and diseases include e.g. eating disorders, obesity,
 CC bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss,
 CC epileptic seizures, migraine, sleep disturbance, pain,
 CC sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage,
 CC shock, congestive heart failure, nasal congestion or diarrhoea. (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-236; Indels 0; Gaps 0;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFYSKQDYNMDELEDEYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60
 DB 1 MSFYSKQDYNMDELEDEYNNKTATENTTAATRNDFPVDYKSSVDDQYFLIGLYTF 60
 QY 61 VSLGFMGNLLILMALMKRKNQKTTNVLGNLAFSDILVLFCSPPFLTSLVLDQWFG 120
 DB 61 VSLGFMGNLLILMALMKRKNQKTTNVLGNLAFSDILVLFCSPPFLTSLVLDQWFG 120
 QY 121 KVMCHIMPLOCVSVLVSTLILISAIIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
 DB 121 KVMCHIMPLOCVSVLVSTLILISAIIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240
 DB 181 CSPLPVHSLVLOETFGSALLSSRYLCSVPWSDSYRIATISLLVQYILPLVCLTVS 240
 QY 241 HTSVCRSISCGLSNKENLEENINLTLPKSKGPOVKLSGSHKWSYFIKXRRYS 300
 DB 241 HTSVCRSISCGLSNKENLEENINLTLPKSKGPOVKLSGSHKWSYFIKXRRYS 300
 QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLPHVTTDFDNDNLISNRHFKLVYCIC 420

Db 361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420

Qy 421 HLLGMSCCLNPILYGLFNGGKADLVSLIHLCHM 455
Db 421 HLLGMSCCLNPILYGLFNGGKADLVSLIHLCHM 455

RESULT 3
ID AAW29413 standard; protein; 455 AA.
XX AAW29413;
XX 25-MAR-2003 (revised)
DT 24-FEB-1998 (first entry)
XX Human hippocampal neuropeptide Y Y5 receptor.

XX Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis;
KW bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss;
KW epileptic seizure; migraine; sleep disturbance; pain; depression;
KW sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea;
KW congestive heart failure; eating disorder; obesity.

XX Homo sapiens.
XX WO9720820-A1.
XX 12-JUN-1997.

XX 16-NOV-1996; 96WO-BP005055.
XX 01-DEC-1995; 95US-00566349.
XX (NOVS) NOVARTIS AG.

XX Rueger H, Schmidlin T, Rigollier P, Yamaguchi Y;
PI Tintelnotblomley M, Schilling W, Criscione L;
XX WFI; 1997-319711/29.
DR N-PSDB; AAT89110.

XX Use of new and known heteroaryl compounds as NPY Y5-receptor antagonists
PT - for treating and preventing eating disorders, diabetes, dyslipidaemia,
PT hypertension, memory loss, epilepsy, migraine, etc.
XX Disclosure; Page 76-78; 155pp; English.

XX This sequence represents human hippocampal neuropeptide (NP) Y receptor
CC subtype Y5, with a pharmacological function associated with for example,
CC obesity and eating disorders. The specification relates to a method of
CC treatment and prophylaxis of disorders and diseases associated with
CC NPY receptor subtype Y5 comprising administering to a warm-blooded
CC animal, including man, in need of such treatment a therapeutically
CC effective amount of a new heteroaryl compound. These disorders and
CC diseases include e.g. eating disorders, obesity, bulimia nervosa,
CC diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
CC migraine, sleep disturbance, pain, sexual/reproductive disorders,
CC depression, anxiety, cerebral haemorrhage, shock, congestive heart
CC failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-236;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFYSKQDYNMDELDEYVYKTLATENNNTAATNSDFPWWDDYKSSVDDLOVELIGLYTF 60
Db 1 MSFYSKQDYNMDELDEYVYKTLATENNNTAATNSDFPWWDDYKSSVDDLOVELIGLYTF 60

Qy 61 VSLIGFMGNLLILMALMKRNOKTWNFLIGNLAFSDILVLFCSPTLTSVLDDQWFG 120
Db 61 VSLIGFMGNLLILMALMKRNOKTWNFLIGNLAFSDILVLFCSPTLTSVLDDQWFG 120
Qy 121 KWCHIMPELQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGPFI 180
Db 121 KWCHIMPELQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYELIATVMTLGPFI 180
Qy 181 CSPLPVFHSVLQETFGSALSSRYLQVSWPSDSYEAFTISILAVQYILPLVCLTVS 240
Db 181 CSPLPVFHSVLQETFGSALSSRYLQVSWPSDSYEAFTISILAVQYILPLVCLTVS 240
Qy 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGQVQLSGHKMSYSFIKRRRYS 300
Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGQVQLSGHKMSYSFIKRRRYS 300
Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCEIKPEENSVDHEL 360
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQVPTCEIKPEENSVDHEL 360
Qy 361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db 361 RVKRSVTRIKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Qy 421 HLLGMSCCLNPILYGLFNGGKADLVSLIHLCHM 455
Db 421 HLLGMSCCLNPILYGLFNGGKADLVSLIHLCHM 455

RESULT 4

AAW37093

ID AAW37093 standard; protein; 455 AA.

XX AAW37093;
XX 08-JUN-1998 (first entry)

XX Homo sapiens hippocampal Y5 receptor.

XX Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity;
XX feeding behaviour; modification; atypical neuropeptide.

XX Homo sapiens.
XX WO9746250-A1.

XX 11-DEC-1997.

XX 04-JUN-1997; 97WO-US009504.

XX 21-FEB-1997; 96US-00668650.

XX 21-FEB-1997; 97US-00803600.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Gerald CP, Weinshank RL, Walker MW, Branchek T;
PI WFI; 1998-051901/05.

XX N-PSDB; AAV00622.

XX DNA encoding canine hypothalamic atypical neuro-peptide Y/peptide YY
PT receptor, Y5 - useful for identification of compounds which are capable
PT of modifying feeding behaviour.

XX Disclosure; Fig 6; 273pp; English.

XX The sequence is that of a hippocampal Y5 receptor (Y5-R). Y5-R can be
CC used in processes to determine whether a chemical compound specifically
CC binds to and activates or inhibits a Y5-R by measuring a second messenger
CC response. The chemical compounds can be used to increase or reduce the
CC activity of a Y5-R. In particular, inhibitors can be used to treat
CC obesity and activators can be used to treat anorexia. Antagonists capable
CC of alleviating (by decreasing the activity of Y5-R) an abnormality can be

CC identified by administering a potential antagonist to a transgenic mammal
 CC as above, and determining whether the substance alleviates the physical
 CC and behavioural abnormalities displayed by the transgenic mammal as a
 CC result of overactivity of a Y5-R. Agonists can be identified in a similar
 CC manner, but where the abnormality is alleviated by increasing the
 CC activity of Y5-R
 XX
 SQ Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSQDYNMDELDEYNNKTLATENTTAATNSDFFPWDDYKSSVDDLOQVFLGLYTF 60
 DB 1 MSFYSQDYNMDELDEYNNKTLATENTTAATNSDFFPWDDYKSSVDDLOQVFLGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNOKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120
 DB 61 VSLGFMGNLLILMALMKRNOKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180

QY 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 DB 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYS 300
 DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYS 300

QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQGVPTCTCFIKEPENS DVHEL 360
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQGVPTCTCFIKEPENS DVHEL 360

QY 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420
 DB 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455
 DB 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 5
 AAY57461
 ID AAY57461 standard; protein; 455 AA.

AC AAY57461;

XX 25-FEB-2000 (first entry)

DE Human hippocampal Y5 receptor.

XX Y5 receptor; feeding behaviour; food consumption; obesity; bulimia;
 KW anorexia; neuropeptide; genetic engineering.

XX Homo sapiens.

XX US968819-A.

XX 19-OCT-1999.

XX 01-DEC-1995; 95US-00566096.

XX 02-DEC-1994; 94US-00349025.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Walker MW, Branchek T, Gerald CPG, Weinshank RL;

XX

DR WPI; 1999-590415/50.
 DR N-PSDB; AAZ39046.
 XX Nucleic acid encoding a human neuropeptide Y receptor useful in genetic engineering.

XX Disclosure; Fig 6; 87pp; English.

CC The present sequence represents the human hippocampal Y5 receptor. The Y5
 CC receptor is a G-protein coupled neuropeptide Y receptor found throughout
 CC the mammalian nervous system and is a powerful stimulant of feeding
 CC behaviour. Cells expressing DNA encoding the Y5 receptor can be used to
 CC determine whether a ligand specifically binds to a Y5 receptor. These
 CC cells or a cell extract, is exposed to the ligand and then any binding
 CC between the ligand and the receptor can be detected. The cells can also
 CC be used to determine whether a ligand is a Y5 receptor antagonist or
 CC agonist. The binding of chemical compounds to a Y5 receptor can also
 CC determined and whether they activate or inhibit the activation of the Y5
 CC receptor can also be determined using cells expressing the receptor. The
 CC effect of drugs on the Y5 receptor and whether they act as agonists or
 CC antagonists can also be detected with these cells

XX Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-236;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSQDYNMDELDEYNNKTLATENTTAATNSDFFPWDDYKSSVDDLOQVFLGLYTF 60
 DB 1 MSFYSQDYNMDELDEYNNKTLATENTTAATNSDFFPWDDYKSSVDDLOQVFLGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNOKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120
 DB 61 VSLGFMGNLLILMALMKRNOKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWVFG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180

QY 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 DB 181 CSPLPVFHSVLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYS 300
 DB 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYS 300

QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQGVPTCTCFIKEPENS DVHEL 360
 DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIQGVPTCTCFIKEPENS DVHEL 360

QY 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420
 DB 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVTTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455
 DB 421 HLLGMWSCCLNPILYGFLLNGIKADLVSLIHCLHM 455

RESULT 6

AAE08002
 ID AAE08002 standard; protein; 455 AA.

XX AAE08002;

XX 01-NOV-2001 (first entry)

XX Human neuropeptide Y5 (NPY5) receptor.

XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
 KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;

PT Modifying feeding behavior of subject, useful in treating feeding
PT disorders, involves administering to subject Y5 receptor agonist or
PT antagonist, to increase or decrease consumption of food by subject.
XX
XX
XX Claim 53; Fig 6; 102pp; English.
XX
XX This invention describes a novel method of modifying feeding behaviour of
CC a subject which involves administering to the subject an amount of a
CC compound which is a Y5 receptor agonist or antagonist effective to
CC increase or decrease, respectively, the consumption of food by the
CC subject so as to modify feeding behaviour of the subject. The product of
CC the invention has metabolic, anorectic, antidepressant, tranquiliser,
CC anti-migraine, analgesic, hypotensive, cerebroprotective, cardiac,
CC anti-diarrhoeic and haemostatic activity and can be used in a vaccine. Y5
CC receptor agonist or antagonist compounds are useful for treating a
CC feeding disorder (e.g. anorexia, obesity or bulimia) in a subject. The
CC pharmaceutical compositions described in the disclosure are useful for
CC treating an abnormality alleviated by the inhibition or activation of Y5
CC receptor, in a subject. Antibodies raised against the receptor are useful
CC for detecting the presence of the receptor on the surface of a cell. The
CC agonist of Y5 receptor is useful for treating an abnormality in a
CC subject, where the abnormality includes anorexia, sexual/reproductive
CC disorder, depression, anxiety, memory loss, migraine, pain, epileptic
CC seizure, hypertension, cerebral haemorrhage, shock, congestive heart
CC failure, sleeve disturbance, nasal congestion, and diarrhoea. This
CC sequence represents the human hippocampus Y5 receptor described in the
CC disclosure of the invention
XX
XX
SQ Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 5; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-236;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60
DB 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60
QY 61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120
DB 61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120
QY 121 KVMCHIMPLOCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAI 180
DB 121 KVMCHIMPLOCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAI 180
QY 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKRRRYS 300
DB 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKRRRYS 300
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360
DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360
QY 361 RVKRSVTRIKRSRSVFRILILVFAVSMPLHLFHVNTDFNDNISNRHFKLVYVCIC 420
DB 361 RVKRSVTRIKRSRSVFRILILVFAVSMPLHLFHVNTDFNDNISNRHFKLVYVCIC 420
QY 421 HLLGWMSCCLNPIYGLFNNNGIKADLVSLIHCLHM 455
DB 421 HLLGWMSCCLNPIYGLFNNNGIKADLVSLIHCLHM 455

RESULT 8
ID ABB79510
ID ABB79510 standard; protein; 455 AA.
XX
AC ABB79510;
XX

DT 23-SEP-2002 (first entry)
XX
DE Human neurotensin Y5 receptor.
XX
XX Neurotensin Y5; NPV; NPV5; receptor; human; antagonist; anorectic;
KW anti-inflammatory; nootropic; neuroprotective; cardiovascular;
KW hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiac;
KW cerebroprotective; antidepressant; haemostatic; tranquilizer;
KW neuroleptic; analgesic; anti-anxiety; nephrotropic; uropathic;
KW gastrointestinal; antiasthmatic.
OS Homo sapiens.
XX
XX WO200248152-A2.
XX
XX 20-JUN-2002.
XX
XX 11-DEC-2001; 2001WO-US047863.
XX
XX 12-DEC-2000; 2000US-0254990P.
XX
XX (NEUR-) NEUROGEN CORP.
XX
XX Bakthavatchalam R, Blum CA, Briemann HU, Darrow JW;
PI De Lombaert S, Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;
XX
XX WPI: 2002-547845/58.
XX
XX N-PSDE; AEN84252.
XX
XX New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or 3H-
PT spiro(isobenzofuran-1,4'-piperidine, useful for treating, e.g. eating
PT disorder, psychiatric, cardiovascular disorder or diabetes.
XX
XX Example 675; Page 129-130; 134pp; English.
XX
XX The present sequence is the protein sequence for the human neurotensin
CC Y5 (NPV5) receptor. In an example from the invention, chimeric receptors
CC including human NPV5 receptor sequences were constructed, and used to
CC assay the binding activity of compounds of the invention. Substituted
CC spiro(isobenzofuran-1,4'-piperidin)-3-ones and 3H-spiro(isobenzofuran-1,4'-
CC piperidines capable of modulating NPV5 receptor activity are provided.
CC Such compounds may be used to modulate ligand binding to NPV5 receptors
CC in vivo or in vitro, and are particularly useful in the treatment of a
CC variety of disorders, e.g. eating disorders such as obesity or bulimia,
CC psychiatric disorders, diabetes and cardiovascular disorders such as
CC hypertension, in humans and animals
XX
SQ Sequence 455 AA;

Query Match 100.0%; Score 2385; DB 5; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-236;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60
DB 1 MSFYSKQDYNMDELDYVYKTLATENNNTAATRNSTDFPVDYKSSVDLQYFLGLYTF 60
QY 61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120
DB 61 VSLGFMGNLLILMALMKRQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120
QY 121 KVMCHIMPLOCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAI 180
DB 121 KVMCHIMPLOCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAI 180
QY 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240
DB 181 CSPLPVPHSLVLOETFGSALLSRYLCSVPSPDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKRRRYS 300
DB 241 HTSVCRSISCGLSNKENLEENINLTLPSPKSGQVQLSGHKWSYFIKRRRYS 300

QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFETKPEENSVDHEL 360
DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFETKPEENSVDHEL 360
QY 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420
DB 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420
QY 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHCLHM 455
DB 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHCLHM 455

RESULT 9
AAO23266
ID AAO23266 standard; protein; 455 AA.
XX AC AAO23266;
DT 25-SEP-2003 (first entry)
DE Human neuropeptide Y5 receptor (NPY5) protein.
KW Neuropeptide Y5; receptor; NPY5; 2-cyclohexyl-4-phenyl-1H-imidazole; NPY;
KW appetite regulation; feeding disorder; obesity; bulimia; diabetes;
KW psychiatric; cardiovascular; hypertension; cerebral infarction; epilepsy;
KW schizophrenia; depression; angina; sudden cardiac death; vasospasm;
KW arrhythmia; urinary incontinence; Crohn's disease; asthma; neuroleptic;
KW antiinflammatory; nootropic; vasotropic; anticonvulsant; uropathic;
human.
OS Homo sapiens.
XX PN EPI306085-A1.
XX PD 02-MAY-2003.
XX PF 21-OCT-2002; 2002EP-00023469.
XX PR 23-OCT-2001; 2001US-0348974P.
XX PA (NEUR-) NEUROGEN CORP.
XX PI Blum CA, Brielmann HL, De Lombaert S, Zheng X;
XX N-PSDB; AAL56583.
XX PS New 2-cyclohexyl-4-phenyl-1H-imidazole derivatives are modulators of
neuropeptide Y5 receptor activity, useful for treating e.g. eating or
psychiatric disorders.
XX Example 10; Page 39-41; 63pp; English.
XX This invention relates to novel ligands (derivatives of 2-cyclohexyl-4-
phenyl-1H-imidazole) for the neuropeptide Y5 (NPY5) receptor. The NPY5
receptor mediates a variety of physiological effects and is involved in
appetite regulation, hormone release and blood pressure. Ligands that
modulate the NPY5 receptor inhibit or enhance NPY binding such that they
can be used to treat a variety of conditions including feeding disorders
(obesity and bulimia), psychiatric disorders, diabetes and cardiovascular
diseases such as hypertension. Further uses relate to the treatment of
cerebral infarction, epilepsy, schizophrenia, depression, angina, sudden
cardiac death, vasospasm, arrhythmia, urinary incontinence, Crohn's
disease and asthma. As such these ligands can be described variously as
neuroleptic, antiinflammatory, nootropic, vasotropic, anticonvulsant and
uropathic. This polypeptide sequence is the human neuropeptide Y5 (NPY5)
receptor protein of the invention

Query Match 100.0%; Score 2385; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-236;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFYSQDYNNMOLEDEYNNKTLATENNNTAATRNSDPFWDDYKSSVDDLOVFLGLYTF 60
DB 1 MSFYSQDYNNMOLEDEYNNKTLATENNNTAATRNSDPFWDDYKSSVDDLOVFLGLYTF 60
QY 61 VSLILGFWGNLLIIMALKKRNOKTTVNFILIGNLAFSDILVLFQSPFTLTSLVLLDQWFG 120
DB 61 VSLILGFWGNLLIIMALKKRNOKTTVNFILIGNLAFSDILVLFQSPFTLTSLVLLDQWFG 120
QY 121 KVMCHIMPLOQCVSVLVSTLILISIAIVRYHMKPIISNNLTANHGFIATVWTLGFAI 180
DB 121 KVMCHIMPLOQCVSVLVSTLILISIAIVRYHMKPIISNNLTANHGFIATVWTLGFAI 180
QY 181 CSPLPVFHSILVELQETFGSALLSSRYLCVESWPSDSYRIAPTISILLVQYILPLVCLTVS 240
DB 181 CSPLPVFHSILVELQETFGSALLSSRYLCVESWPSDSYRIAPTISILLVQYILPLVCLTVS 240
QY 241 HTSVCSISICGLSNKENRLEENEMINLTHPSKSGPQVKLSSGSHKWSYISFKHRRYS 300
DB 241 HTSVCSISICGLSNKENRLEENEMINLTHPSKSGPQVKLSSGSHKWSYISFKHRRYS 300
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFETKPEENSVDHEL 360
DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFETKPEENSVDHEL 360
QY 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420
DB 361 RVKRSVTRIKKRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYIC 420
QY 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHCLHM 455
DB 421 HLLGMSCCCLNPILYGLFNNGIKADLVSLIHCLHM 455

RESULT 10
ADO29564
ID ADO29564 standard; protein; 455 AA.
XX AC ADO29564;
DT 29-JUL-2004 (first entry)
DE Human GPCR NPY5R, SEQ ID NO:666.
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianemic; antiepileptic;
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
receptor.
OS Homo sapiens.
XX PN WO2004040000-A2.
XX PD 13-MAY-2004.
XX PF 09-SEP-2003; 2003WO-US028226.
XX PR 09-SEP-2002; 2002US-0409303P.
XX PR 09-APR-2003; 2003US-0461329P.
XX PA (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vaesiliatis D, Zeng H;
XX WPI: 2004-390329/36.
DR N-PSDB; ADO30001.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 666; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 455 AA;
SQ
Query Match 100.0%; Score 2385; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-236; Indels 0; Gaps 0;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFYSKQDYNMDELDEYNNKTLATENNATATNSDFPVDYKSSVDDQLQYFLGYTF 60
DB 1 MSFYSKQDYNMDELDEYNNKTLATENNATATNSDFPVDYKSSVDDQLQYFLGYTF 60
QY 61 VSLGLFMGNLILMALMKRKNQKTVNPLGNLAFSLIVLFCSPPTLSVLLDQWFG 120
DB 61 VSLGLFMGNLILMALMKRKNQKTVNPLGNLAFSLIVLFCSPPTLSVLLDQWFG 120
QY 121 KVMCHIMPFLOQSVLVSTLILISIAIVRYHMKIPHSNNLTANHGYFLIATVTLGFAI 180
DB 121 KVMCHIMPFLOQSVLVSTLILISIAIVRYHMKIPHSNNLTANHGYFLIATVTLGFAI 180
QY 191 CSPLPVHSLVELQTFQSALLSRVLCVSWPDSYRIAPTISLLVQILPVLCLTVS 240
DB 191 CSPLPVHSLVELQTFQSALLSRVLCVSWPDSYRIAPTISLLVQILPVLCLTVS 240
QY 241 HTSVCRSISCSGLSKENRLEENEMINTLHPKSKSGQVXLGSHKWSYFIKHHRRYS 300
DB 241 HTSVCRSISCSGLSKENRLEENEMINTLHPKSKSGQVXLGSHKWSYFIKHHRRYS 300
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360

DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360
QY 361 RVKRSVTRIKKRSRVFYRLTILILVPAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
DB 361 RVKRSVTRIKKRSRVFYRLTILILVPAVSMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
QY 421 HLLGMSCCCLNPLYGFLNNGIKADLVSLIHCLHM 455
DB 421 HLLGMSCCCLNPLYGFLNNGIKADLVSLIHCLHM 455
RESULT 11
AAE08016
ID AAE08016 standard; protein; 455 AA.
XX AC AAE08016;
XX 01-NOV-2001 (first entry)
XX African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.
XX Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW locomotor; anxiety disorder; limbic disorder; tranquilliser;
KW african green monkey; AGM.
XX Cercopithecus aethiops.
XX WO200155103-A2.
XX 02-AUG-2001.
XX 29-JAN-2001; 2001WO-US002804.
XX 28-JAN-2000; 2000US-0178652P.
XX (NEUR-) NEUROGEN CORP.
XX Bennett M, Brodbeck R, Krause J;
XX WPI; 2001-514543/56.
XX N-PSDB; AAD14746.
XX New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
PT discovery and development.
XX Example 2; Page 70-72; 72pp; English.
XX The present invention relates to chimeric neuropeptide Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with seven
CC membrane spanning transmembrane (TM) domains. The compounds that modulate
CC the activity of a NPY receptor is useful in the preparation of a
CC medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPY5 receptor may have an anti-epileptic activity in the
CC control of limbic seizures. The present sequence is african green monkey
CC (AGM) NPY5 receptor
XX Sequence 455 AA;
Query Match 99.5%; Score 2373; DB 4; Length 455;
Best Local Similarity 99.3%; Pred. No. 2.1e-235;
Matches 452; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSFYSKQDYNMDELDEYNNKTLATENNATATNSDFPVDYKSSVDDQLQYFLGYTF 60
DB 1 MSFYSKQDYNMDELDEYNNKTLATENNATATNSDFPVDYKSSVDDQLQYFLGYTF 60

QY 61 VSLGFGWGNLILMALMKKRNOKTIVNFIAGNLAFLSDILVLPFCSPFTLSVLLDQWFG 120
 DB 61 VSLGFGWGNLILMALMKKRNOKTIVNFIAGNLAFLSDILVLPFCSPFTLSVLLDQWFG 120
 QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFAL 180
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFAL 180
 QY 181 CSPLPVFHSVLVQLQETFGSALLSRYLCVSWPDSYRIAFITISLLLVQVILPLVCLTVS 240
 DB 181 CSPLPVFHSVLVQLQETFGSALLSRYLCVSWPDSYRIAFITISLLLVQVILPLVCLTVS 240
 QY 241 HTSVCRSISCGLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFPIKRRRYS 300
 DB 241 HTSVCRSISCGLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFPIKRRRYS 300
 QY 301 KKTACVLPAPEPPOENHSRILPENFGSVRQLSSSKFIPGVPTCTEIKPEENSVDYHEL 360
 DB 301 KKTACVLPAPEPPOENHSRILPENFGSVRQLSSSKFIPGVPTCTEIKPEENSVDYHEL 360
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 DB 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 QY 421 HLLGWMSCCLNPILYGLFNNGIKADLVSLIHCLHM 455
 DB 421 HLLGWMSCCLNPILYGLFNNGIKADLVSLIHCLHM 455

RESULT 12
 AAW27604
 ID AAW27604 standard; protein; 445 AA.
 AC AAW27604;
 XX
 DT 14-APR-1998 (first entry)
 DE Human neuropeptide Y receptor (NPY Y5).
 KW Neurotansmitter; antagonist; agonist; obesity; anorexia;
 KW hyperlipidaemia; diabetes; gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO9737998-A2.
 XX
 PD 16-OCT-1997.
 XX
 PF 08-APR-1997; 97WO-US005781.
 XX
 PR 08-APR-1996; 96US-0014969P.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Hu Y, McCaleb ML, Bloomquist BT, Flores-Riveros JR, Cornfield LJ;
 XX
 DR WPI; 1997-512637/47.
 DR N-PSDB; AAT73602.
 XX
 PT Nucleic acid molecule encoding neuro:peptide Y receptor - useful to
 PT identify antagonists and agonists, e.g. treat obesity, diabetes,
 PT hyperlipidaemia and anorexia.
 XX
 PS Claim 2; Page 37-39; 49pp; English.
 XX
 CC A novel human receptor for the neurotransmitters neuropeptide Y (NPY) and
 CC peptide YY (PYY) is designated NPY Y5 receptor. Its amino acid sequence
 CC was deduced from a human genomic DNA clone (see AAT7940). Rat NPY Y5 has
 CC also been identified (see AAW27602-03). These polypeptides can be
 CC expressed in host (e.g. human 293) cells. The effects of NPY include
 CC blood pressure regulation, memory enhancement, anxiolysis/sedation and
 CC increased food intake. The receptor can therefore be used to screen for

CC antagonists and agonists capable of controlling these conditions;
 CC antagonists could be used to treat obesity and diabetes by reducing
 CC appetite and food consumption, while agonists could be used to treat
 CC anorexia
 CC
 XX Sequence 445 AA;
 QY
 Query Match 97.7%; Score 2330; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 5.5e-231;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 MDLEDEYKNTLATENNTAATNSDPYWDYKSDVDDLOVFLGLGYTFVLLGFMGNL 70
 DB 1 MDLEDEYKNTLATENNTAATNSDPYWDYKSDVDDLOVFLGLGYTFVLLGFMGNL 50
 QY 71 LILMALMKKRNOKTIVNFIAGNLAFLSDILVLPFCSPFTLSVLLDQWFGKVMCHIMPFL 130
 DB 61 LILMALMKKRNOKTIVNFIAGNLAFLSDILVLPFCSPFTLSVLLDQWFGKVMCHIMPFL 120
 QY 131 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCPLPVFHS 190
 DB 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGFLIATVMTLGFALCPLPVFHS 180
 QY 191 VELQETFGSALLSRYLCVSWPDSYRIAFITISLLLVQVILPLVCLTVSHTSVCRSIS 250
 DB 181 VELQETFGSALLSRYLCVSWPDSYRIAFITISLLLVQVILPLVCLTVSHTSVCRSIS 240
 QY 251 GLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFPIKRRRYSKKTACVLPA 310
 DB 241 GLSNKENRLEENEMINLTLPSSKSGQVQLSGSHKWSYFPIKRRRYSKKTACVLPA 300
 QY 311 ERPSQENHSRILPENFGSVRQLSSSKFIPGVPTCTEIKPEENSVDYHELVRKSVTRIK 370
 DB 301 ERPSQENHSRILPENFGSVRQLSSSKFIPGVPTCTEIKPEENSVDYHELVRKSVTRIK 360
 QY 371 KRGRSVFVRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGWMSCCL 430
 DB 361 KRGRSVFVRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGWMSCCL 420
 QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455
 DB 421 NPILYGLFNNGIKADLVSLIHCLHM 445
 RESULT 13
 AAW15230
 ID AAW15230 standard; protein; 445 AA.
 XX
 AC AAW15230;
 XX
 DT 21-JUL-1997 (first entry)
 DE Human neuropeptide Y-Y5 receptor.
 XX
 KW Neuropeptide Y-Y5; appetite; obesity; G-protein coupled receptor;
 KW antiobesity; hypotensive; neuronal growth factor; cardiovascular drug;
 KW anti-psychotic; neuroleptic; antidiabetic; agonist; antagonist.
 XX
 OS Homo sapiens.
 XX
 PN WO9717440-A1.
 XX
 PD 15-MAY-1997.
 XX
 PF 08-NOV-1996; 96WO-AU000706.
 XX
 PR 09-NOV-1995; 95AU-00006467.
 XX
 PA (GARV-) GARVAN INST MEDICAL RES.
 XX
 PI Herzog H;
 XX
 DR WPI; 1997-281029/25.

DR N-PSDB; AAT66909, AAT66910.
 XX DNA encoding the neuro-peptide Y-Y5 receptor - for screening for NPY-Y5
 PT antagonists and agonists; useful as anti-obesity agents, anti-
 PT hypertensive agents cardiovascular drugs, etc.
 XX
 XX Claim 17; Fig 1; 44pp; English.
 XX
 XX A novel human neuropeptide Y (NPY)-Y1-like receptor (AAW15230),
 CC designated NPY-Y5 receptor, is a G-protein coupled receptor of NPY, which
 CC is involved in appetite/obesity regulation. Its amino acid sequence was
 CC deduced from isolated genomic (AAT66909) and foetal brain cDNA (AAT66910)
 CC sequences. Rat (AAW15232) and mouse (AAW15233) NPY-Y5 receptors have also
 CC been identified. NPY-Y5 receptors can be expressed on the cell surface of
 CC host (pref. CHO, human embryonic kidney 293 or insect Sf9) cells. The
 CC receptors or host cells can be used to screen for NPY (ant)agonists
 CC useful as potential hypotensives, cardiovascular drugs, neuronal growth
 CC factors, anti-psychotic, anti-obesity or anti-diabetic drugs
 XX
 XX Sequence 445 AA;

Query Match 97.7%; Score 2330; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 5.5e-231;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNNTAATNSDPFVDDYKSSVDDLOQLFLGLYTFVSLGFMGNL 70
 Db 1 MDLEDEYNNKTLATENNNTAATNSDPFVDDYKSSVDDLOQLFLGLYTFVSLGFMGNL 60
 QY 71 LILMALMKKRNOKTTNFIIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 130
 Db 61 LILMALMKKRNOKTTNFIIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 120
 QY 131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSPVPVHSL 190
 Db 121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSPVPVHSL 180
 QY 191 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISILLVQYILPLVCLTVSHTSVCRSISC 250
 Db 181 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISILLVQYILPLVCLTVSHTSVCRSISC 240
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPQVKSGLSHKWSYFIKKHRRYSKKTACVLPAP 310
 Db 241 GLSNKENRLEENEMINLTLPKSKSGPQVKSGLSHKWSYFIKKHRRYSKKTACVLPAP 300
 QY 311 ERPSQENHSRIILPENFGSVRSOLSSSSKEIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
 Db 301 ERPSQENHSRIILPENFGSVRSOLSSSSKEIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 430
 Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 420
 QY 431 NPILYGFLNNGIKADLVSLIHCLHM 455
 Db 421 NPILYGFLNNGIKADLVSLIHCLHM 445

RESULT 14
 AAY14554
 ID AAY14554 standard; protein; 445 AA.
 XX
 AC AAY14554;
 XX
 XX 31-AUG-1999 (first entry)
 XX Human neuropeptide Y5 receptor protein.
 XX
 XX Human; neuropeptide Y; NPY; receptor; hypothalamus; antagonist; agonist;
 KW obesity; diabetes; antibody; detection.
 XX
 OS Homo sapiens.
 XX

PN US5919901-A.
 XX
 PD 06-JUL-1999.
 XX
 PF 08-APR-1996; 96US-00630118.
 XX
 PR 08-APR-1996; 96US-00630118.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Cornfield LJ, Flores-Riveros JR, Hu Y, Mccaleb ML, Bloomquist BT;
 XX
 XX WPI; 1999-394648/33..
 DR N-PSDB; AAX83197.
 XX
 XX Neuropeptide Y receptor Y5 and related nucleic acid.
 XX
 XX Claim 3; Col 29-34; 23pp; English.
 XX
 XX This sequence represents the human neuropeptide Y5 receptor (Y5) protein.
 CC The protein is useful for screening for compounds able to be used as
 CC agonists and antagonists to the Y5 receptor, especially for the treatment
 CC obesity and diabetes and for developing antibodies for the detection of
 CC the protein
 XX
 XX Sequence 445 AA;

Query Match 97.7%; Score 2330; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 5.5e-231;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNNTAATNSDPFVDDYKSSVDDLOQLFLGLYTFVSLGFMGNL 70
 Db 1 MDLEDEYNNKTLATENNNTAATNSDPFVDDYKSSVDDLOQLFLGLYTFVSLGFMGNL 60
 QY 71 LILMALMKKRNOKTTNFIIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 130
 Db 61 LILMALMKKRNOKTTNFIIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPF 120
 QY 131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSPVPVHSL 190
 Db 121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVTLGFAICSPVPVHSL 180
 QY 191 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISILLVQYILPLVCLTVSHTSVCRSISC 250
 Db 181 VELOETFGSALLSSRYLCVESWPSDSYRTAFTISILLVQYILPLVCLTVSHTSVCRSISC 240
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPQVKSGLSHKWSYFIKKHRRYSKKTACVLPAP 310
 Db 241 GLSNKENRLEENEMINLTLPKSKSGPQVKSGLSHKWSYFIKKHRRYSKKTACVLPAP 300
 QY 311 ERPSQENHSRIILPENFGSVRSOLSSSSKEIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
 Db 301 ERPSQENHSRIILPENFGSVRSOLSSSSKEIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 430
 Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGWMSCCL 420
 QY 431 NPILYGFLNNGIKADLVSLIHCLHM 455
 Db 421 NPILYGFLNNGIKADLVSLIHCLHM 445

RESULT 15
 AAY52578
 ID AAY52578 standard; protein; 445 AA.
 XX
 AC AAY52578;
 XX
 XX 28-FEB-2000 (first entry)
 XX Human NPY (neuropeptide Y) Y5 receptor.
 DE

XX Neuropeptide Y; NPY; receptor; Y5; G-protein coupled; expression;
KW chimeric; pharmacological property; peripheral nervous system;
KW central nervous system; physiological; activity; food intake; feeding;
KW thermogenesis; blood pressure; hormone release; gut motility;
KW smooth muscle tone; sleep; circadian rhythm; neuronal excitability;
KW nociception; mood; emotional response; seizure activity; diuresis;
KW natriuresis; calcitriol; antinase; agonist; antagonist; obesity;
KW hypertension; epilepsy; sexual dysfunction; jet lag.
XX Homo sapiens.
OS
XX US9595616-A.
XX 16-NOV-1997.
XX 07-JAN-1998; 98US-00003199.
XX 07-JAN-1998; 98US-00003199.
XX (SCHE) SCHERING CORP.
XX Parker EM, Rudinski MS, Strader CD;
XX WPI; 2000-012792/01.
XX N-PSDB; AAZ46232.
XX Chimeric mammalian neuropeptide Y5 receptor polypeptides useful for
PT treating a range of disorders including jet lag, hypertension and sexual
XX dysfunction.
XX Example; Col 37-40; 24pp; English.
XX This sequence represents human neuropeptide Y (NPY) Y5 receptor, cDNA
CC encoding which was isolated and amplified from a human neuroblastoma cell
CC line using primers AAZ46215-246223. The receptor was transiently
CC expressed in COS1 cells, but its level of expression was found to be
CC significantly lower in comparison to that of the rat NPY Y5 receptor
CC (AAV52579). The invention relates to a chimeric rat/human NPY receptor,
CC comprising the 5' untranslated region (5' UTR) and extreme 5' coding
CC region (105 bp) of the rat Y5 receptor cDNA, appended to nucleotides 365-
CC 1633 of the human Y5 receptor cDNA. When transfected into COS1 cells, the
CC chimeric construct yielded levels of expression higher than the native
CC human Y5 receptor, and similar or greater levels of expression than the
CC native rat Y5 receptor. The pharmacological properties of the chimeric
CC receptor were similar to those of the native human Y5 receptor. NPY is
CC widely distributed in both the peripheral and central nervous systems and
CC has a wide range of physiological activities including effects on food
CC intake, thermogenesis, blood pressure, hormone release, gut motility,
CC smooth muscle tone, sleep and circadian rhythms, neuronal excitability,
CC nociception, mood and emotional responses. NPY mediates these
CC physiological effects via interactions with at least six distinct G-
CC protein coupled receptors (designated Y1-Y6). The Y5 receptor mediates
CC the effects of NPY on feeding, thermogenesis, neuronal excitability and
CC seizure activity, diuresis, natriuresis and calcitriol. The chimeric Y5
CC receptor, associated nucleic acids (e.g., expression vectors or antisense
CC molecules), agonists or antagonists may be administered to treat
CC disorders such as obesity, hypertension, epilepsy, sexual dysfunction and
CC jet lag associated with abnormal expression/activity of NPY
XX
SQ Sequence 445 AA;

Query Match 97.7%; Score 2330; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 5.5e-231;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNATATNSDFPWWDDYKSSVDDLOYLFLIGLYTFVSLGFMGNL 70
DB 1 MDLEDEYNNKTLATENNATATNSDFPWWDDYKSSVDDLOYLFLIGLYTFVSLGFMGNL 60
QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFMGKVMCHIMPFL 130
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFMGKVMCHIMPFL 120

QY 131 QCVSVLSTLILISIAIVRHYMKHPISNNLTANHGFLIATVMTGLFAICSPPLVFHSL 190
DB 121 QCVSVLSTLILISIAIVRHYMKHPISNNLTANHGFLIATVMTGLFAICSPPLVFHSL 180
QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIATISLLVQYILPLVCLTVSHTSVCRSTSC 250
DB 181 VELOETFGSALLSSRYLCVESWPSDSYRIATISLLVQYILPLVCLTVSHTSVCRSTSC 240
QY 251 GLSNKENLEENEMINLTLPSSKSGPOVKLSGSHKWSYSPFKHRRYSKKTACVLPAP 310
DB 241 GLSNKENLEENEMINLTLPSSKSGPOVKLSGSHKWSYSPFKHRRYSKKTACVLPAP 300
QY 311 ERPSQENHSRILPENFGSVRSQSSSKXFIPOVTCFBIKPEENSDVHELVRKSVTEIK 370
DB 301 ERPSQENHSRILPENFGSVRSQSSSKXFIPOVTCFBIKPEENSDVHELVRKSVTEIK 360
QY 371 KRSRSVFYRLTILILFAVSWMPLHLFHVTDNDNLISNRHFKLVYICHLGLGMSCLL 430
DB 361 KRSRSVFYRLTILILFAVSWMPLHLFHVTDNDNLISNRHFKLVYICHLGLGMSCLL 420
QY 431 NPILYGFLLNGIKADLVSLIHCLHM 455
DB 421 NPILYGFLLNGIKADLVSLIHCLHM 445

Search completed: October 21, 2004, 12:09:59
Job time : 156 secs

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OM protein - protein search, using sw model

Run on: October 21, 2004, 11:59:55 : Search time 40 Seconds
(without alignments)
1094.466 Million cell updates/sec

Title: US-09-771-956-13
Perfect score: 2385
Sequence: 1 NSGYSKQDYNMDELDEYNN.....GFLNNGIKADLVSLHGLHM 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	481.5	20.2	366	S71152	neuropeptide Y/pep
2	481.5	20.2	384	A45490	neuropeptide Y/pep
3	480	20.1	349	S12863	G protein-coupled
4	480	20.1	382	B41333	neuropeptide Y/pep
5	480	20.1	382	S27388	neuropeptide Y/pep
6	464.5	19.5	375	I32182	pancreatic polypep
7	463.5	19.4	375	G02300	neuropeptide Y rec
8	458	19.2	375	S63685	neuropeptide Y rec
9	455.5	19.1	381	I39187	neuropeptide Y/pep
10	404	16.9	370	I52315	G protein-coupled
11	384	16.1	584	JC7809	sulfakinin recepto
12	377	15.8	436	JC5599	cholecystokinin-A
13	375	15.7	427	S00150	gastric CCK-A rece
14	368.5	15.5	444	A42685	cholecystokinin re
15	367	15.4	449	A41738	neuropeptide Y rec
16	356	14.9	428	JN0692	cholecystokinin ty
17	355.5	14.9	430	I51898	cholecystokinin A
18	351.5	14.7	447	A47430	gastrin/cholecysto
19	347	14.5	455	T15622	hypothetical prote
20	343.5	14.4	453	S32817	gastrin receptor -
21	339.5	14.2	452	JC2459	gastrin/cholecysto
22	329.5	13.8	450	JQ1614	gastrin receptor -
23	329.5	13.8	452	A46195	cholecystokinin B
24	320	13.4	423	B40470	glucocorticoid-ind
25	316.5	13.3	457	T29741	hypothetical prote
26	309.5	13.0	423	JC7677	allatostatin recep
27	308.5	12.9	394	JC7209	galanin receptor -
28	306.5	12.9	365	T20184	hypothetical prote
29	303	12.7	399	T16277	hypothetical prote

RESULT 1

S71152

neuropeptide Y/peptide YY receptor Y1 - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S71152; S55924

R;Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.

submitted to the EMBL Data Library, November 1993

A;Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenop

A;Reference number: S71152

A;Accession: S71152

A;Molecule type: mRNA

A;Residues: 1-366 <NAR>

A;Cross-references: UNIPROT:P34992; EMBL:L25416; NID:G409169; PIDN:AAA49918.1; PID:G4091

A;Experimental source: brain, hypothalamus

R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.

Biochim. Biophys. Acta 1261, 439-441, 1995

A;Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA fr

A;Reference number: S55924; NCID:95260870; PMID:7742373

A;Accession: S55924

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-278,'T',280-366 <BLO>

A;Cross-references: EMBL:L25416; NID:G409169

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.2%; Score 481.5; DB 2; Length 366;

Best Local Similarity 26.4%; Pred. No. 6e-31;

Matches 114; Conservative 75; Mismatches 128; Indels 115; Gaps 8;

QY	19	YNKTLATENTNTAATNSDPFVWDYKSSVDDQLQVFLGL-YTFVSLGLFGMGNLLILMALM 77
Db	6	YFENISVPNNISG-NITFPISDCALPLP-MFTLALAYCAVILGLSGLNLILIL 61
QY	78	KRNQKNTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHIMPFCQSVLV 137
Db	62	KQKERNVTNIIIVNLVSFSDLLATMCLPFTLIYTLMDHWFGEVCKLNEYIQCVSV 121
QY	138	STLILISIAIVRYHMKHPISNNLTANHYFLIATVTLGFAICSLPVPHSLVLEQTF 197
Db	122	SIFSVLIAIEHQILINPRGWRPNRACGIVINGFANACSTPLMVMYSVLTD--EPP 179
QY	198	GSALLSS---RYLCVESWPSDSYRIAFITISLLVQYLPLVCLTVSHTSVCRISCSLSN 254
Db	180	KNISLDSVIGKVCYCLEDFEDKFRISYTTLLFIQLGLFCIFVCYTKI----- 229
QY	255	KENRLEENEMINLTLPKSGPQVKLSGSHKWSVFIFKHRRYSKKTACVLPAPERPS 314
Db	230	-----FRLKRR----- 236
QY	315	QENHGRILPENFGSVRSQJSSSSKPIGVPCTCFEIKPEENSVDVHLEKVSVTRIKRSR 374

```

Db      237 -----NMMDKLRDNKYRSSETKR-- 255
QY      375 SVFYRLTILILFAVSWMLPLHPLHVVDNDNLISNRHFKLVYICICHLGMMSCCLNPIIL 434
Db      256 -INIMLLSVGWGFAFLFFIPNLVFDWNHEAVATCNHLLFLICHLTAMISTCWNPIF 314
QY      435 YGFLNNGIKADL 446
Db      315 YGFLNKNFORDL 326

RESULT 2
A45490
neuropeptide Y/peptide YY receptor Y1 - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A45490; A46133; A42773
R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A:Title: Genomic organization, localization, and allelic differences in the gene for the
A:Reference number: A45490; MUID:93203272; PMID:8095935
A:Accession: A45490
A:Molecule type: DNA
A:Residues: 1-384 <HER>
A:Cross-references: UNIPROT:P25929; GB:L07615; NID:G189284; PIDN:AAA59947.1; PID:G189285
A>Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBI:P:128000)
R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A:Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: A46133
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-384 <HE2>
A>Note: sequence extracted from NCBI backbone (NCBI:P:108538)
R:Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlstedt, C.
J. Biol. Chem. 267, 10938-10938, 1992
A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
A:Reference number: A42773; MUID:92283782; PMID:1317848
A:Accession: A42773
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-384 <LA6>
A:Cross-references: GB:M88461; NID:G189155; PIDN:AAA73215.1; PID:G189156
A:Experimental source: fetal brain
A>Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBI:P:104736)
C:Genetics:
A:Gene: GDB:NPV1R; NPYR
A:Cross-references: GDB:132643; OMIM:162641
A:Map position: 4q31.3-4q32
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F:37-66/Domain: transmembrane #status predicted <TM1>
F:77-103/Domain: transmembrane #status predicted <TM2>
F:118-136/Domain: transmembrane #status predicted <TM3>
F:155-179/Domain: transmembrane #status predicted <TM4>
F:209-232/Domain: transmembrane #status predicted <TM5>
F:261-286/Domain: transmembrane #status predicted <TM6>
F:300-323/Domain: transmembrane #status predicted <TM7>
F:113-198/Disulfide bonds: #status predicted
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match      20.2%; Score 481.5; DB 2; Length 384;
Best Local Similarity 26.3%; Pred. No. 6.4e-31;
Matches 115; Conservative 76; Mismatches 129; Indels 117; Gaps 8;

QY      20 NKTLL--ATENNTA----ATRNDFPVDYDKSSVDDQLQYFLIGL-YTFVSLGFMGNLLI 72
Db      2 NSTLFSQVNHSHVSNFSEKNAQLAFENDCHLPLAMITFLALAYGAVILGVSGNLAL 61
QY      73 LMALMKRNQKTTNVLNGLAFSDILVLFCS9FTLTSVLLQWFGKVNCHIMPFLQ 132

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Db      62 IIIILKQKRNVTNLIIVNLFSDDLVAIMCLPFTFYVTLMDHWVFGEMACKLNPFVQC 121
QY      133 VSLVSTLIILISIAVRYRMKHPISNNLTANHGFLIATVTLGFAICSPLEVFHSLVE 192
Db      122 VSTISVFSVLVLIARHQLIINPRGWRPNRHHAYGVIAVWL--AVASSLPFLYQVM 179
QY      193 LQETFGSALLSS--RYLCVESWSPSSYRTAFTISILLVQYILPLVCLTVSHTSVCRSIS 249
Db      180 TDEPFQNVTLDAYDKYVCFDQFSPDSHRLSYTLTLLVLYQYFGFLCFIFICYFKI 234
QY      250 CGLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYRYSKKTACVLPA 309
Db      235 -----YRLKRR----- 241
QY      310 PERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHELVRKSVTRI 369
Db      242 -----NNMDKMRDNKYRSSE 257
QY      370 KESRSVYFRLTILILFAVSWMLPLHPLHVVDNDNLISNRHFKLVYICICHLGMMSCC 429
Db      258 TKR---INIMLLSVGWGFAFLFFIPNLVFDWNHEAVATCNHLLFLICHLTAMISTC 314
QY      430 LNPILYGLNNGIKADL 446
Db      315 VNPIFYGLNKNFORDL 331

RESULT 3
S12863
G protein-coupled receptor FCS - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S12863; S19101
R:Eva, C.; Keinenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
A:Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the
A:Reference number: S12863; MUID:91032093; PMID:2172008
A:Accession: S12863
A:Molecule type: mRNA
A:Residues: 1-349 <EVA>
A:Cross-references: UNIPROT:P21555; EMBL:Z11504
R:Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
A:Description: Pharmacological and Transduction Properties of a Recombinantly Expressed
A:Reference number: S19101
A:Accession: S19101
A:Molecule type: mRNA
A:Residues: 1-343; DDYETIAMSTWHTDVSKTSLKQASPVAFKLSVNDNEKI' <KRA>
A:Cross-references: EMBL:Z11504; NID:G57636; PIDN:CAA77579.1; PID:G57637
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:73-93/Domain: transmembrane #status predicted <TM1>
F:114-135/Domain: transmembrane #status predicted <TM2>
F:155-175/Domain: transmembrane #status predicted <TM3>
F:213-231/Domain: transmembrane #status predicted <TM4>
F:262-285/Domain: transmembrane #status predicted <TM5>
F:299-322/Domain: transmembrane #status predicted <TM6>
F:2,11,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match      20.1%; Score 480; DB 2; Length 349;
Best Local Similarity 25.9%; Pred. No. 7.5e-31;
Matches 114; Conservative 74; Mismatches 127; Indels 126; Gaps 9;

QY      20 NKTLL--ATENNTA----ATRNDFPVDYDKSSVDDQLQYFLIGLYTF-----VSLGFMG 68
Db      2 NSTLFSRVNYSVHVNSNSPFLAFEN----DCHLPLAVITFLALAYGAVILGVSG 56
QY      69 NLLIILMALMKRNQKTTNVLNGLAFSDILVLFCS9FTLTSVLLQWFGKVNCHIMP 128
Db      57 NLLIILKOKMRNVTNLIIVNLFSDDLVAIMCLPFTFYVTLMDHWVFGEMACKLN 116

```

QY 129 FLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGXYFLIATVMTLGFALICSPLPVFH 188
 Db 117 FVQCVSITVSIFSLVIAVERHQIINPGWPNRHHAYIGITVIAVLAVASSLPFVIYQ 176
 QY 189 SLVELOETFGSALLS---RYLCVESWPSDSVRIAFITSLLDVQYILPLVCLTVSHTSVC 245
 Db 177 ILTD--EPFQNVSLAAFKDKYVCFDPKPSDSHRLSYTTLLLVQYFGPLCFIFICYFKI- 233
 QY 246 RSISCGLSNKENLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTAC 305
 Db 234 -----YRLKRRNNMMDK----- 246
 QY 306 VLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHELVRKRS 365
 Db 247 -----IRDSKYRSSE----- 256
 QY 366 VTRIKKRSRVFRLTILILVAVSWMPHLPHVVTDFNDNLISNRHFKLVYVCICHLGGM 425
 Db 257 -----TKRINMLLSIVVAFVAVCWLPITFNTVFDNHNHQLIATCNHNLFLCHLTAM 309
 QY 426 MSCCLNPILYGFNLNGIKADL 446
 Db 310 ISTCVNPIFYGFNLKNFQDRL 330

RESULT 4

B46133
 C;Species: Mus musculus (house mouse)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
 C;Accession: B46133
 R;Herzog, H.; Hott, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
 A;Title: Cloned human neurotensin Y receptor couples to two different second messenger
 A;Reference number: A46133; MUID:92335184; PMID:1321422
 A;Accession: B46133
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-382 <HER>
 A;Note: sequence extracted from NCBI backbone (NCBIP:108539)
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 20.1%; Score 480; DB 2; Length 382;
 Best Local Similarity 25.9%; Pred. No. 8.4e-31;
 Matches 114; Conservative 74; Mismatches 127; Indels 126; Gaps 9;

QY 20 NKTLL--ATENNTA---ATNSDPVWDYKSSVDDLYQLYGLTYF-----VSLDGMG 68
 Db 2 NSTLFRVENYSHYVNSNSPLAPEN-----DCHLPLAVIPLTALAYGAVIILVSG 56
 QY 69 NLAILMALMKRNQKTTNPLNLAFLSDILVLFCSPTLTSLVLLDQMGKVMCHIMP 128
 Db 57 NLALIIILKOKEMRVNVTNLIWNLSFSDLLVAVMCLPPTFVYTLMDHWFGETMCKLNP 116
 QY 129 FLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGXYFLIATVMTLGFALICSPLPVFH 188
 Db 117 FVQCVSITVSIFSLVIAVERHQIINPGWPNRHHAYIGITVIAVLAVASSLPFVIYQ 176
 QY 189 SLVELOETFGSALLS---RYLCVESWPSDSVRIAFITSLLDVQYILPLVCLTVSHTSVC 245
 Db 177 ILTD--EPFQNVSLAAFKDKYVCFDPKPSDSHRLSYTTLLLVQYFGPLCFIFICYFKI- 233
 QY 246 RSISCGLSNKENLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTAC 305
 Db 234 -----YRLKRRNNMMDK----- 246
 QY 306 VLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHELVRKRS 365
 Db 247 -----IRDSKYRSSE----- 256
 QY 366 VTRIKKRSRVFRLTILILVAVSWMPHLPHVVTDFNDNLISNRHFKLVYVCICHLGGM 425

Db 257 -----TKRINMLLSIVVAFVAVCWLPITFNTVFDNHNHQLIATCNHNLFLCHLTAM 309
 QY 426 MSCCLNPILYGFNLNGIKADL 446
 Db 310 ISTCVNPIFYGFNLKNFQDRL 330

RESULT 5

S27388
 C;Species: Mus musculus (house mouse)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S27388
 R;Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.
 FEBS Lett. 314, 285-288, 1992
 A;Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex
 A;Reference number: S27388; MUID:93106169; PMID:1468559
 A;Accession: S27388
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-382 <EVA>
 A;Cross-references: UNIPROT:Q04573; EMBL:Z18280; NID:G53438; PIDN:CAA79157.1; PID:G53439
 C;Superfamily: neurokinin 1 receptor

Query Match 20.1%; Score 480; DB 2; Length 382;

Best Local Similarity 25.9%; Pred. No. 8.4e-31;
 Matches 114; Conservative 75; Mismatches 126; Indels 126; Gaps 9;
 QY 20 NKTLL--ATENNTA---ATNSDPVWDYKSSVDDLYQLYGLTYF-----VSLDGMG 68
 Db 2 NSTLFRVENYSHYVNSNSPLAPEN-----DCHLPLAVIPLTALAYGAVIILVSG 56
 QY 69 NLAILMALMKRNQKTTNPLNLAFLSDILVLFCSPTLTSLVLLDQMGKVMCHIMP 128
 Db 57 NLALIIILKOKEMRVNVTNLIWNLSFSDLLVAVMCLPPTFVYTLMDHWFGETMCKLNP 116
 QY 129 FLOCVSVLSTLLISIAIVRYHMKHPISNNLTANHGXYFLIATVMTLGFALICSPLPVFH 188
 Db 117 FVQCVSITVSIFSLVIAVERHQIINPGWPNRHHAYIGITVIAVLAVASSLPFVIYQ 176
 QY 189 SLVELOETFGSALLS---RYLCVESWPSDSVRIAFITSLLDVQYILPLVCLTVSHTSVC 245
 Db 177 ILTD--EPFQNVSLAAFKDKYVCFDPKPSDSHRLSYTTLLLVQYFGPLCFIFICYFKI- 233
 QY 246 RSISCGLSNKENLEENEMINLTLPSSKSGQVQLSGSHKWSYFIKKHRRYSKKTAC 305
 Db 234 -----YRLKRRNNMMDK----- 246
 QY 306 VLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHELVRKRS 365
 Db 247 -----IRDSKYRSSE----- 256
 QY 366 VTRIKKRSRVFRLTILILVAVSWMPHLPHVVTDFNDNLISNRHFKLVYVCICHLGGM 425
 Db 257 -----TKRINMLLSIVVAFVAVCWLPITFNTVFDNHNHQLIATCNHNLFLCHLTAM 309
 QY 426 MSCCLNPILYGFNLNGIKADL 446
 Db 310 ISTCVNPIFYGFNLKNFQDRL 330

RESULT 6

I39182
 C;Species: Homo sapiens (man)
 C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: I39182
 R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.
 J. Biol. Chem. 270, 26762-26765, 1995
 A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic
 A;Reference number: I39182; MUID:96070761; PMID:7592911
 A;Accession: I39182


```

Best Local Similarity 24.9%; Pred. No. 1.7e-22;
Matches 109; Conservative 84; Mismatches 175; Indels 70; Gaps 13;

QY 23 LATENNTAATFSDPPVWDYKSSVDDLOQVFLGLTYTFVSLGFMGNLLILMALMKRQ 82
Db 20 LGLNETFLCLODQOPS-KEWQAVQIL-----LYSFILSLVLGTLVITVLIRKRW 72
QY 83 KTVNFNLGNLAFSDILAVLFCSPFTLTSVLLDQWFGKVMCHIMPFLOCVSVLSTLIL 142
Db 73 RTVTINIFLLSLAVSDMLCLFCMPFNLIPLLKDFIFGSAVCKTTTYFMGTSVSVSTENL 132
QY 143 ISTAIRVYHMIKPIISNNL--TANHGCVLIATVWTGLFAICSPLPVPHSLVELQETFGSA 200
Db 133 VASLERYGAICPLQSRVWQTKSHALKVIAAWCLSFITMTPEYISLVLPFTKNNQT 192
QY 201 LLSSRYLCVESWPSDSYRIAFITSLLVQVILPLVCLTVSHTSCVRSISGILSNKENRLE 260
Db 193 ANWCRFL-----PSDAQSQWQTFLLILFLIPGVVMVAYGLISLELQGKFDASQ-- 246
QY 261 ENEMINUTLHPSKSGPQVKLS---GSHKWSYFIKRRRRYSKKTACVLPAPERPSQEN 317
Db 247 -----KSAKEKFLSSGGGGGSSS-----SRYEDSDGCLQKSRPPKLE 288
QY 318 HSRILPENFGVSQSLSSSSKFIPGVPCTFEIKPEENS DVHELVRKSVTRIKRSRVF 377
Db 289 -----LQQLSTSS-----SGGRINIRSSGSANLIAKR-VI 320
QY 378 YRUTLILVAVSWMLPHLHVVTDFNDNLISNRHFK---LVYICHLGLMMSCCLNPLIL 434
Db 321 RMLIVIVLWFLFCWMPIFSANAWRAY-DTVSAEKHLSGTPISPIL--LLSYTSSCVNPII 377
QY 435 YGFLNNGIKADLVSLIHC 452
Db 378 YCFMNRKFRGLGFMAFPFC 395

RESULT 13
S50150
gastric CCK-A receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
C;Accession: S50150
R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
Biochim. Biophys. Acta 1219, 321-327, 1994
A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.
A;Reference number: S50150; MUID:95002144; PMID:7918628
A;Accession: S50150
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <REU>
C;Superfamily: neurokinin 1 receptor

Query Match 15.7%; Score 375; DB 2; Length 427;
Best Local Similarity 25.7%; Pred. No. 2.5e-22;
Matches 104; Conservative 73; Mismatches 155; Indels 72; Gaps 9;

QY 57 LYTFVSLGFMGNLLILMALMKRQKTTVNPFLIGNLAFSDILVVLFCSPFTLTSVLLDQ 116
Db 47 LYSILFLLSLVLGTLVITVLIRKMRVTVTNIFLLSLAISDLMLCLFCMPFNLIENLLKD 106
QY 117 WNFQKVMCHIMPFLOCVSVLSTLLISIAIVRYHMIKPIISNNL--TANHGCVLIATVW 174
Db 107 FIFGSAKCTTTTYLMGTSVSVSTLNLVAISERYGAICKPLQSRVWQTKSHALKVIAATW 166
QY 175 TLGFAICGPLPVPHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFITSLLVQVILPL 234
Db 167 CLSFALMTPEYISLVLPFTKNNQTANWCRFL-----PSDVMQAWHTFLLLILFLIPG 222
QY 235 VCLTVSHTSCVRSISGILSNKENRLEENEMINLTHPSKSGPQVKLSGSHKWSYFTKK 294
Db 223 IYVMWAY-----GMTSLELYQG-----IKFDASQKKS-----AK 251
QY 295 HRR-----RYSKKTACVLPAPERPSQENHSRIILPENFGSVRSOLSSSKFIPGVPCTFE 348

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Db 252 ERKASTGSGFEDNDCYLQR-SKPTQLEQLQOLSGGGGRVSRHSS----- 298
QY 349 IKEPENSVDHLEVRKSRVTRIKRSRVSRYRITLILVAVSWPLHUFHVVTDFNNLI 408
Db 299 -----SSAALNAKRRVIRM-----LNVITVLFLLCWMPIFSANAWRAYDTVSA 342
QY 409 SNRHPKLVVYICHLGMSCLNPIYGLFLNNGIKADLVSLIHC 452
Db 343 ERLSGTPTLFFILLSYTSVCNPIYCFMNRFLGFWATPFC 386

RESULT 14
A42685
Cholecystokinin receptor type A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Accession: A42685; J04225; F02213
R;Wank, S.A.; Watkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slattey, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 3125-3129, 1992
A;Title: Purification, molecular cloning, and functional expression of the cholecystokinin
A;Reference number: A42685; MUID:92212981; PMID:1313582
A;Accession: A42685
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-444 <MAN>
A;Cross-references: UNIPROT:P30551; GB:M88096; NID:9203383; PID:G203384
A;Experimental source: pancreas
A;Note: Sequence extracted from NCBI backbone (NCBI:93814, NCBI:P:93815)
R;Takata, Y.; Takiguchi, S.; Funakoshi, A.; Kono, A.
Biochem. Biophys. Res. Commun. 213, 958-966, 1995
A;Title: Gene structure of rat cholecystokinin type-A receptor.
A;Reference number: J04225; MUID:95382845; PMID:7654260
A;Accession: J04225
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-223 <TAK>
A;Cross-references: DDBJ:D50608; NID:G1100752
R;Mantamadiotis, T.; Baldwin, G.S.
Biochem. Biophys. Res. Commun. 201, 1382-1389, 1994
A;Title: The seventh transmembrane domain of gastrin/CKK receptors contributes to non-pe
A;Reference number: PC2213; MUID:94296413; PMID:8024583
A;Accession: PC2213
A;Status: preliminary
A;Molecule type: protein
A;Residues: 366-389 <MAN>
C;Comment: This G-protein-coupled receptor is present in the gastrointestinal system, va
ducing the subsequent release of intracellular calcium.
C;Genetics:
A;Gene: CKKAR
A;Introns: 53/1; 137/1; 224/2; 267/1
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
F;57-82/Domain: transmembrane #status predicted <TM1>
F;93-119/Domain: transmembrane #status predicted <TM2>
F;131-151/Domain: transmembrane #status predicted <TM3>
F;173-193/Domain: transmembrane #status predicted <TM4>
F;225-249/Domain: transmembrane #status predicted <TM5>
F;330-348/Domain: transmembrane #status predicted <TM6>
F;366-389/Domain: transmembrane #status predicted <TM7>

Query Match 15.5%; Score 368.5; DB 2; Length 444;
Best Local Similarity 24.3%; Pred. No. 8.5e-22;
Matches 106; Conservative 86; Mismatches 17; Indels 73; Gaps 12;

QY 23 LATENTATRNDFPVDYDSSVDDIQLYFLIGLYTFVSLILGFGNLLIIMALKRNRQ 82
Db 35 LGLENETFLCLOQPS-KWQSALQIL-----LYSIFLLSVLGNLTIVTLIRNKR 87
QY 83 KITWNEFLNAPSDILVLFPCSPFTLTSVLLDWMFGKVMCHIMPFQCQSVLVSLIIL 142
Db 88 RTVTNIFLSLAVSLMLCLFCWPNLNLKDFISAVCKTTFWMTGTSVSTFNL 147

QY 143 ISIAIVRHMKHPISNNL--TANHGYPILATVTLGFAICSPILPVHSLVLOETFGSA 200
Db 148 VAISLERGAICRPQSRVQWTKSHALYIAATWCLSTIMTPYIENLVFFTKNNQT 207
QY 201 LLSSRYLCVESPPSDSYRIAFETISILLVQYILPLVCLTVSHTSVCRISCGLSNKRLE 260
Db 208 ANMCRFL-----PSDAMQSQWTFLLILFLPLGIVMVAVGLISLELYQGIKFDASQ-- 261
QY 261 ENEMINLTHPSKSKSPQVKLS-QSHKWSYSFIKHHRRYSKKTACVLPAPERFSQENHS 319
Db 262 -----KSAKCKPSTGS-----STRYEDSDGCVLQSKRPKRLEQL 298
QY 320 RILPENFGSVRSQSSSKSIFPGVPTCFEIKPEENSDVHELVRKSRVTRIKRSRSVFYR 379
Db 299 QLSSGGSGSLNRIRSS-----SSAANLIARVRM----- 330
QY 380 LILILLVAVSWPLHUFHVVTDFNNLISNRHFK--LVYICHLGMSCLNPIYLG 436
Db 331 LIVIVLFLCWMPIFSANAWRAY-DTVAEKHLSGTPIFIL--LLSYTSSCNPIIYC 387
QY 437 FLNNGIKADLVSLIHC 452
Db 388 FMNKRFLGFWATPFC 403

RESULT 15
A41738
neuropeptide Y receptor - fruit fly (Drosophila melanogaster)
N;Alternate names: G protein-coupled receptor PR4
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41738
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.
J. Biol. Chem. 267, 9-12, 1992
A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide 1
A;Reference number: A41738; MUID:92112730; PMID:1370455
A;Accession: A41738
A;Molecule type: mRNA
A;Residues: 1-449 <LIA>
A;Cross-references: UNIPROT:P25931; GB:M81490; NID:G157996; PID:AAA28727.1; PID:G157997
C;Genetics:
A;Gene: FlyBase:Nepyr
A;Cross-references: FlyBase:FBgn0004842
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 15.4%; Score 367; DB 2; Length 449;
Best Local Similarity 22.8%; Pred. No. 1.1e-21;
Matches 99; Conservative 66; Mismatches 123; Indels 146; Gaps 12;

QY 41 DDYKSSVDDL---QYFLI---GLYTFVSLGFGNLLIIMALKRNRQKTTVNLIGNLA 94
Db 74 DDYDLLEDMMSSAYFKIIVMLYIPIFALIGNTVCVIVYVSTPRMRTVNYFIASLA 133
QY 95 FSDILVLFPCSPFTLTSV-LLDWMFGKVMCHIMPFQCQSVLVSLTILISIAIVRYHMI 153
Db 134 IGDILMSFCEPSSFISFILNYWPFGLALCHFNYSQAVSLVSAVTLVAISIDRIVAI 193
QY 154 KHPISNNITANHGYPILATVTLGFAICSPILV-----FHSVLVEQETFGSALLS 203
Db 194 MWPLPRITKRYATFIAGVWFIALATALPIPIVSGLDIPMSPHTKCE----- 242
QY 204 SYLCVSWSPSDSYRIAFETISILLVQYILPLVCLTVSHTSVCRISCGLSNKRLEENE 263
Db 243 -KYICREWSPRSQBYTYTLLSFLALQVPLGVLFYARITRV----- 286
QY 264 MTNLTLPKSKSGPOVKLSGSHKWSYSFIKHHRRYSKKTACVLPAPERFSQENHSRLP 323
Db 287 -----WA-----KRP----- 291
QY 324 ENFGSVRSQSSSKSIFPGVPTCFEIKPEENSDVHELVRKSRVTRIKRSRSVFRLTIL 383

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Db      292 -----PG-----EATNRDQMARSKRKQVKM-----MLTV 317
QY      384 ILVFAVSWPLHLFHVVTDFNDNLISNRHF-----KLVYICICHLGMMSCCLNPILYGF 437
Db      318 VIVFTCCWLPFNILQL-----LNDEEFHWDPLPYVWFHFLAMSHCCYNPIIYCY 370
QY      438 LNNGIKADLVSLIH 451
Db      371 MNARFRSGFVQLMH 384

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Search completed: October 21, 2004, 12:14:03
 Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2004, 11:57:55 ; Search time 192 Seconds
(without alignments)
1363.518 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385
Sequence: 1 MGFSQKDYNDLEDEYN.....GFLNNGIKADLVSLHCLHM 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2385	100.0	455	1	Q15761 homo sapien
2	2330	97.7	445	2	Aah42416
3	2318	97.2	445	2	Q9GK73 macaca mula
4	2241	94.0	446	2	Q925F1
5	2227	93.4	446	1	Q63729 canis famil
6	2084	87.4	456	1	Q63634 rattus norv
7	2070	86.8	466	1	O70342 mus musculu
8	2070	86.8	466	2	Bac32426 mus muscu
9	2028	85.0	446	1	Q97969 sus scrofa
10	1629	5	68.3	443	Q8dfm2 gallus gall
11	558	23.4	377	2	O73733
12	527	22.1	348	2	Q6Y6A4
13	527	22.1	348	2	AA062565
14	522	21.9	373	2	Q6Y6A5
15	522	21.9	373	2	AA062564
16	502	21.1	377	2	Q8QSM3
17	497	20.8	371	1	Q6Y6A4
18	487	20.4	382	1	Q6Y6A5
19	487	20.4	383	1	Q6Y6A4
20	484	20.3	395	1	Q8QPM1
21	481	20.2	366	1	Q6Y6A5
22	481	20.2	366	1	Q6Y6A4
23	481	20.2	384	1	Q6Y6A5
24	481	20.2	384	2	AA062564
25	481	20.2	384	2	AAH71720
26	481	20.2	383	1	Q6Y6A4
27	480	20.1	382	1	Q6Y6A5
28	480	20.1	382	1	Q6Y6A4
29	480	20.1	382	2	AAH51420
30	476	20.0	371	1	Q6Y6A5
31	476	20.0	371	2	Bac26875

32	473.5	19.9	385	1	NY2R_CHICK	Q9cdn6	gallus gall
33	471	19.7	374	2	Q9YHX1	Q9Yhx1	gadus morhu
34	466	19.5	375	2	Q9Y505	Q9Y505	sus scrofa
35	464.5	19.5	375	1	NY4R_HUMAN	P50391	homo sapien
36	464.5	19.5	375	2	Q6FH06	Q6Fh06	homo sapien
37	464	19.5	375	1	NY4R_RAT	O53447	rattus norv
38	463.5	19.4	375	2	O574E3	O57463	brachydanio
39	462	19.4	375	2	Q6YHV0	Q6Yhvo	macaca mula
40	462	19.4	375	2	AA028939	AA028939	macaca mu
41	459	19.2	371	2	Q6Y6A6	Q6Y6a6	squalus aca
42	459	19.2	371	2	AA062563	AA062563	squalus aca
43	458.5	19.2	381	2	Q8BWV1	Q8bwv1	mus musculu
44	458.5	19.2	385	1	NY2R_MOUSE	P97295	mus musculu
45	458	19.2	375	1	NY4R_MOUSE	Q61041	mus musculu

ALIGNMENTS

RESULT 1

ID	NY5R_HUMAN	STANDARD	PRT	455 AA
AC	Q15761; Q92916;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPY5)			
GN	Name=NPY5R; Synonyms=NPYR5;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hippocampus; PubMed=8700207;			
RX	MEDLINE=96317589; PubMed=8824284;			
RA	Batzl-Hartmann C., Walker M.W., Criscione L., Gustafson E.L., Taber R.I., Branchek T.A., Weinshank R.L., Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G., Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L., Sadlewski Y., Schaefer J., Velazquez N., McCaleb M.L., "A receptor subtype involved in neuropeptide-Y-induced food intake."			
RL	Nature 382:168-171(1996).			
RN	[2]			
RN	SEQUENCE OF 11-455 FROM N.A.			
RP	MEDLINE=96421636; PubMed=8824284;			
RX	Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B., Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L., Sadlewski Y., Schaefer J., Velazquez N., McCaleb M.L., "Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior."			
RL	J. Biol. Chem. 271:26315-26319(1996).			
RN	[3]			
RP	SEQUENCE OF 11-455 FROM N.A.			
RX	MEDLINE=9712686; PubMed=9169127;			
RA	Harzog H., Darby K., Ball H., Hort Y., Beck-Sickinger A., Shine J., "Overlapping gene structure of the human neuropeptide Y receptor subtypes 11 and 15 suggests coordinate transcriptional regulation."			
RL	Genomics 41:315-319(1997).			
RN	[4]			
RP	SEQUENCE OF 11-455 FROM N.A.			
RA	Kopatz S.A., Aronstam R.S., Sharma S.V., "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases			
CC	-1- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: Brain; hypothalamus.			
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.			

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CC or send an email to license@isb-sib.ch).

EMBL; U56079; AAC50623.1; -
EMBL; U66275; AAC50741.1; -
EMBL; U94320; AAC51295.1; -
EMBL; AY322538; AAP84351.1; -
Genew; HGNC:7958; NPV5R.
MIM; 602001; -
GO; GO:000887; C:integral to plasma membrane; TAS.
GO; GO:0004983; P:neuropeptide y receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
InterPro; IPR000276; GPCR Rhodopsn.
InterPro; IPR000393; NPV5_receptor.
InterPro; IPR000611; NPV_receptor.
Pfam; PF00001; 7tm1; 1.
PRINTS; PR00237; GPCR RHODOPSIN.
PROSITE; PS00237; G-PROTEIN RECP F1.1; FALSE_NEG.
PROSITE; PS0262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Phosphorylation; Transmembrane
FT DOMAIN 1 50 Extracellular (Potential).
FT TRANSMEM 51 72 1 (Potential).
FT DOMAIN 73 84 Cytoplasmic (Potential).
FT TRANSMEM 85 105 2 (Potential).
FT DOMAIN 106 125 Extracellular (Potential).
FT TRANSMEM 126 147 3 (Potential).
FT DOMAIN 148 167 Cytoplasmic (Potential).
FT TRANSMEM 168 188 4 (Potential).
FT DOMAIN 189 220 Extracellular (Potential).
FT TRANSMEM 221 242 5 (Potential).
FT DOMAIN 243 378 Cytoplasmic (Potential).
FT TRANSMEM 379 401 6 (Potential).
FT DOMAIN 402 414 Extracellular (Potential).
FT TRANSMEM 415 438 7 (Potential).
FT DOMAIN 439 455 Cytoplasmic (Potential).
FT CARBOHYD 20 20 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 27 27 N-linked (GlcNAc. . .) (Potential).
FT DISULFD 124 208 By similarity.
FT LIPID 452 452 S-palmitoyl cysteine (Potential).
SQ SEQUENCE 455 AA; 51990 MW; 95F2747E5F8F7 CRC64;

Query Match 100.0%; Score 2385; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.1e-150;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDEYNNKLTATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTF 60
DB 1 MSFYSKQDYNMDELDEYNNKLTATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTF 60
QY 61 VSLIGFNGNLLILMALMKRKNQKTTNVLGNLAFSDILVFLCSPPTLTSVLLDQWFG 120
DB 61 VSLIGFNGNLLILMALMKRKNQKTTNVLGNLAFSDILVFLCSPPTLTSVLLDQWFG 120
QY 121 KVMCHIMPFLQCVSLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFAL 180
DB 121 KVMCHIMPFLQCVSLVSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFAL 180
QY 181 CSPLPVPHSLVQLQETFGSALLSSRYLCVSWPDSYRIAFITSLLVQVILPLVCLTVS 240
DB 181 CSPLPVPHSLVQLQETFGSALLSSRYLCVSWPDSYRIAFITSLLVQVILPLVCLTVS 240
QY 241 HTSVCRSISCGLSNKENLEENINLTLPKSKSGPQVLSGSHKWSYFIKHHRRYS 300
DB 241 HTSVCRSISCGLSNKENLEENINLTLPKSKSGPQVLSGSHKWSYFIKHHRRYS 300
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPCTCFEIKPENSDVHEL 360

DB 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPCTCFEIKPENSDVHEL 360
QY 361 RVKRSVTRIKRSRVSRYRLTILILFVAVSWMLHLFHVVTDFNDNLINRHHKLVYIC 420
DB 361 RVKRSVTRIKRSRVSRYRLTILILFVAVSWMLHLFHVVTDFNDNLINRHHKLVYIC 420
QY 421 HLLGMSCCCLNPLYGLFNNIGIKADLVSLHCLHM 455
DB 421 HLLGMSCCCLNPLYGLFNNIGIKADLVSLHCLHM 455

RESULT 2
AAH42416 PRELIMINARY; PRT; 445 AA.
ID AAH42416
AC AAH42416
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Neuropeptide Y receptor Y5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schain J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.L.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC042416; AAH42416.1; -
KW Neuropeptide; Receptor.
SQ SEQUENCE 445 AA; 50726 MW; A2B0F3169DBA66BE CRC64;

Query Match 97.7%; Score 2330; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 5.1e-147;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKLTATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTFVSLIGFNGNL 70
DB 1 MDLEDEYNNKLTATENNNTAATRNDFPVWDYKSSVDDLYQFLIGLYTFVSLIGFNGNL 60
QY 71 LILMALMKRKNQKTTNVLGNLAFSDILVFLCSPPTLTSVLLDQWFGKVMCHIMPFL 130
DB 61 LILMALMKRKNQKTTNVLGNLAFSDILVFLCSPPTLTSVLLDQWFGKVMCHIMPFL 120
QY 131 QCVSVLSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFALCSPLPVPHSL 190
DB 121 QCVSVLSTLILISIAIVRYHMKIPISNNLTANHGYFLIATVMTLGFALCSPLPVPHSL 180

Db 121 QCVSVLVSTLIIISIAIVRYHMKHPISNNLTANHGYFLIATVTLGLFAICSPLEVFHSL 180
 QY 191 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 250
 Db 181 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 240
 QY 251 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWYSFIRKRRYSKKTACVLPAP 310
 Db 241 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWYSFIRKRRYSKKTACVLPAP 300
 QY 311 ERPSQNHRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
 Db 301 ARPSLENQRTLPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDAEMVRKSVTRIK 360
 QY 371 KRSRSVYFRTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 430
 Db 361 KRSRSVYFRTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 420
 QY 431 NPILYGLNNGIKADIVSLIHLHM 455
 Db 421 NPILYGLNNGIKADIVSLIHLHM 445

RESULT 5

NYSR CANFA STANDARD; PRT; 446 AA.
 AC 062729;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPY5)
 DE Name=NPY5R; Synonyms=NPY5;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99017379; PubMed=9802393;
 RA Borowsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,
 RA Vaysses P., Branchek T.A., Gerald C.;
 RT "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs";
 RL Regul. Pept. 75:45-53 (1998).
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylyate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykinins receptors.
 CC
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 CC
 CC EMBL; AF049328; AAC7838.1;
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC InterPro; IPR000393; NPY5_Receptor.
 CC InterPro; IPR000511; NPY_Receptor.
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
 CC PROSITE; PS00262; G_PROTEIN_RECP_F2_1;
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane.
 FT DOMAIN 1 40 Extracellular (Potential).
 FT TRANSMEM 41 62 1 (Potential).

FT DOMAIN 63 74 Cytoplasmic (Potential).
 FT TRANSMEM 75 95 2 (Potential).
 FT DOMAIN 96 115 Extracellular (Potential).
 FT TRANSMEM 116 137 3 (Potential).
 FT DOMAIN 138 157 Cytoplasmic (Potential).
 FT TRANSMEM 158 178 4 (Potential).
 FT DOMAIN 179 210 Extracellular (Potential).
 FT TRANSMEM 211 232 5 (Potential).
 FT DOMAIN 233 368 Cytoplasmic (Potential).
 FT TRANSMEM 369 391 6 (Potential).
 FT DOMAIN 392 404 Extracellular (Potential).
 FT TRANSMEM 405 428 7 (Potential).
 FT DOMAIN 429 446 Cytoplasmic (Potential).
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).
 FT DISULFID 114 198 By similarity.
 FT LIPID 442 442 S-palmitoyl cysteine (Potential).
 SQ SEQUENCE 446 AA; 51012 MW; 5CAG8D2FCF5D254A CRC64;
 Query Match 93.4%; Score 2227; DB 1; Length 446;
 Best Local Similarity 94.8%; Pred. NO. 3.7e-140;
 Matches 422; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 11 MDLELDYNNKTLATENTTAATNSDFPVWDDYKSSVDDQLQYFLIGLYTFVSLFGMGL 70
 Db 1 MDLELDYNNKTLATENTTAATNSDFPVWDDYKSSVDDQLQYFLIGLYTFVSLFGMGL 60
 QY 71 LILMALMKRKNQKTVNFIIGNLAFSDILVLFCSPTLTSLVLLQDMFGKVMCHIMPFL 130
 Db 61 LILMALMKRKNQKTVNFIIGNLAFSDILVLFCSPTLTSLVLLQDMFGKVMCHIMPFL 120
 QY 131 QCVSVLVSTLIIISIAIVRYHMKHPISNNLTANHGYFLIATVTLGLFAICSPLEVFHSL 190
 Db 121 QCVSVLVSTLIIISIAIVRYHMKHPISNNLTANHGYFLIATVTLGLFAICSPLEVFHSL 180
 QY 191 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 250
 Db 181 VELQETFGSALLSSRYLCVSPDSYRIAFITISILLVQYILPLVCLTVSHTSVCRSISC 240
 QY 251 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWYSFIRKRRYSKKTACVLPAP 310
 Db 241 GLSNKENRLEENEMINLTLPKSGQVQLSGSKWYSFIRKRRYSKKTACVLPAP 300
 QY 311 ERPSQNHRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
 Db 301 ARPSLENQRTLPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHDMVRNRSIMRIK 360
 QY 371 KRSRSVYFRTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 430
 Db 361 KRSRSVYFRTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGMMSCCL 420
 QY 431 NPILYGLNNGIKADIVSLIHLHM 455
 Db 421 NPILYGLNNGIKADIVSLIHLHM 445

RESULT 6

NYSR RAT STANDARD; PRT; 456 AA.
 AC 063634; P70586;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor).
 DE Name=NPY5R; Synonyms=NPYR5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE=963117589; PubMed=8700207;
RA Gerald C., Walker M.W., Criscione L., Gustafson E.L.,
RA Batzl-Hartmann C., Smith K.E., Vayse P., Durkin M.M., Laz T.M.,
RA Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,
RA Taber R.I., Branche T.A., Weinshank R.L.;
RT "A receptor subtype involved in neurotrophin-induced food intake.";
RL Nature 382:168-171 (1996).
RN [2]
RP SEQUENCE OF 12-456 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98332165; PubMed=9669502;
RA Parker E.M., Babji C.K., Balasubramanian A., Burrier R.E., Guzzi M.,
RA Hamud F., Mukhopadhyay G., Rudinski M.S., Tao Z., Tice M., Xia L.,
RA Mullins D.E., Salisbury B.G.;
RT "G231118 (1129091) and other analogues of the C-terminus of
neurotrophin Y are potent neurotrophin Y1 receptor antagonists and
neurotrophin Y4 receptor agonists.";
RL Eur. J. Pharmacol. 349:97-105 (1998).
RN [3]
RP SEQUENCE OF 12-456 FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98421636; PubMed=8824284;
RA Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,
RA Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,
RA Sadowski Y., Schaefer J., Velazquez N., McCall M.L.;
RT "Identification of a novel hypothalamic neurotrophin Y receptor
associated with feeding behavior.";
RL J. Biol. Chem. 271:26315-26319 (1996).
CC -!- FUNCTION: Receptor for neurotrophin Y and peptide YY. The activity
of this receptor is mediated by G proteins that inhibit adenylylate
cyclase activity. Seems to be associated with food intake. Could
be involved in feeding disorders.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Brain; hypothalamus.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC Highest to tachykinin receptors.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; U56078; AAC52677.1; .
DR EMBL; AF044264; AAC15670.1; .
DR EMBL; U66274; AAC52845.1; .
DR GDB; 3199; NPY5r.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000393; NPY5_receptor.
DR InterPro; IPR000611; NPY_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE; PS00462; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Phosphorylation; Transmembrane.
FT DOMAIN 1 51 Extracellular (Potential).
FT TRANSMEM 52 73 1 (Potential).
FT DOMAIN 74 85 Cytoplasmic (Potential).
FT TRANSMEM 86 106 2 (Potential).
FT DOMAIN 107 126 Extracellular (Potential).
FT TRANSMEM 127 148 3 (Potential).
FT DOMAIN 149 168 Cytoplasmic (Potential).
FT TRANSMEM 169 189 4 (Potential).
FT DOMAIN 190 221 Extracellular (Potential).
FT TRANSMEM 222 243 5 (Potential).
FT DOMAIN 244 278 Cytoplasmic (Potential).
FT TRANSMEM 279 301 6 (Potential).
FT DOMAIN 302 324 Extracellular (Potential).
FT TRANSMEM 325 347 7 (Potential).
FT DOMAIN 348 370 Cytoplasmic (Potential).
FT TRANSMEM 371 393 8 (Potential).
FT DOMAIN 394 416 Extracellular (Potential).
FT TRANSMEM 417 439 9 (Potential).
FT DOMAIN 440 462 Cytoplasmic (Potential).

FT DISULFID 125 209 BY similarity.
FT LIPID 452 452 S-palmitoyl cysteine (Potential).
FT CARBOHYD 21 21 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 456 AA; 51715 MW; 5157ABE341BA707E CRC64;
Query Match 87.4%; Score 2084.5; DB 1; Length 456;
Best Local Similarity 88.2%; Pred. No. 1.1e-130;
Matches 396; Conservative 22; Mismatches 30; Indels 1; Gaps 1;
QY 7 QDYNMDELDYNNKTLATENNATATRNDFPVDYDQSSVDDQVFLGLTYEVSLLGF 66
DB 8 QDSMEFLEEHFNKTFVTENNTAARNAFAWEDYRGSVDDQVFLGLTYEVSLLGF 67
QY 67 MGNLLTLMALMKRNOKTTFNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHI 126
DB 68 MGNLLTLMALMKRNOKTTFNVLGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHI 127
QY 127 MPFLQCVSVLSTLIISIAIVRYHMKHPIINNLTANHGFLIATVWTGLGFAICSPPLV 186
DB 128 MPFLQCVSVLSTLIISIAIVRYHMKHPIINNLTANHGFLIATVWTGLGFAICSPPLV 187
QY 187 FHSVLVELOETFGSALLSSRYLCVSWPDSYRIAFITISLLVQYILPLVCLTVSHTSVCR 246
DB 188 FHSVLVELOETFGSALLSSRYLCVSWPDSYRIAFITISLLVQYILPLVCLTVSHTSVCR 247
QY 247 SISCGLSNKENLEENEMINLTLPKSKGPGQVKGSGHWSYFPIKHHRRYSKKTACV 306
DB 248 SISCGLSNKENLEENEMINLTLPKSKGPGQVKGSGHWSYFPIKHHRRYSKKTACV 307
QY 307 LPAPERPSQENHSRIIPENFGSVRSOLSSSKFIPGVPTCFEIKPEENSVDVHRLVKRSV 366
DB 308 LPAPERPSQENHSRIIPENFGSVRSOLSSSKFIPGVPTCFEIKPEENSVDVHRLVKRSV 366
QY 367 TRIKRSRSYFVRLTILVFAVSMWPLHFLHVVTDFNDNLISNRHFKLVYICHLGLMM 426
DB 367 TRIKRSRSYFVRLTILVFAVSMWPLHFLHVVTDFNDNLISNRHFKLVYICHLGLMM 426
QY 427 SCCLNPLVGLNNGIKADLVSLHCLHM 455
DB 427 SCCLNPLVGLNNGIKADLVSLHCLHM 455
RESULT 7
ID NY5R_MOUSE STANDARD; PRT; 466 AA.
AC O70342; O35380; Q9JMKJ;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5
receptor).
GN Name=Npy5r; Synonyms=Npy5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99017379; PubMed=9802393;
RA Borowsky B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,
RA Vayse P., Branche T.A., Gerald C.;
RT "Molecular biology and pharmacology of multiple NPY Y5 receptor
species homologs.";
RL Regul. Pept. 75:45-53 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Brain;
RA Chen H., Adams S., McWhinnie E., Bayne M., Galski R., Zastawny R.;
RT "Mouse neuropeptide Y Y5 receptor characterized by repeat sequence in
extracellular domain.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97459646; PubMed=9315506; DOI=10.1016/S0005-2736(97)00131-4;
 RA Nakamura M., Yokoyama M., Watanabe H., Matsumoto T.;
 RT "Molecular cloning, organization and localization of the gene for the
 RL mouse neurotrophin-3 receptor.";
 CC Biochem. Biophys. Acta 1328:183-189 (1997).
 CC -!- FUNCTION: Receptor for neurotrophin-3 and peptide YY. The activity
 CC of this receptor is mediated by G proteins that inhibit adenylylate
 CC cyclase activity. Seems to be associated with food intake. Could
 CC be involved in feeding disorders (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Highest to tachykinin receptors.
 CC -----
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 CC -----
 DR EMBL; AF049329; AAC17839.1; -;
 DR EMBL; AF022948; AAB81829.1; -;
 DR EMBL; AB001346; BAA89538.1; -;
 DR MG; MG1:108082; Npy5r.
 DR GO; GO:0016020; C:membrane; IDA.
 DR GO; GO:001602; P:pancreatic polypeptide receptor activity; IDA.
 DR GO; GO:0001601; P:peptide YY receptor activity; IDA.
 DR GO; GO:0007273; P:regulation of synapse; IMP.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000393; NPY5_Receptor.
 DR InterPro; IPR000611; NPY_Receptor.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; FALSE_NEG.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Phosphorylation; Transmembrane.
 FT DOMAIN 1 61 Extracellular (Potential).
 FT TRANSMEM 62 83 1 (Potential).
 FT DOMAIN 84 95 Cytoplasmic (Potential).
 FT TRANSMEM 96 116 2 (Potential).
 FT DOMAIN 117 136 Extracellular (Potential).
 FT TRANSMEM 137 158 3 (Potential).
 FT DOMAIN 159 178 Cytoplasmic (Potential).
 FT TRANSMEM 179 199 4 (Potential).
 FT DOMAIN 200 231 Extracellular (Potential).
 FT TRANSMEM 232 253 5 (Potential).
 FT DOMAIN 254 388 Cytoplasmic (Potential).
 FT TRANSMEM 389 411 6 (Potential).
 FT DOMAIN 412 424 Extracellular (Potential).
 FT TRANSMEM 425 448 7 (Potential).
 FT DOMAIN 449 466 Cytoplasmic (Potential).
 FT TRANSMEM 467 499 8 (Potential).
 FT LIPID 462 462 S-palmitoyl cysteine (Potential).
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 195 195 L -> F (in Ref. 1).
 FT CONFLICT 284 284 K -> Q (in Ref. 3).
 SQ SEQUENCE 466 AA; 52784 MW; B157F236F2D4385 CRC64;

Query Match 86.8%; Score 2070; DB 1; Length 466;
 Best Local Similarity 85.2%; Pred. No. 1.1e-129;
 Matches 397; Conservative 23; Mismatches 24; Indels 22; Gaps 2;
 QY 11 MDLEDEYNNKTLATNNAT-----RNSDFPVDYKSSVD 49
 DB 1 MEVKLEHFNKTFVTENNTAASQNTASPAWEDYRGTEENTSAARNTAFPVWEDYRGSSVD 60
 QY 50 LQYFLIGLYTFVSLGLFGMGNLLILMAVMKKNQKTTVNFIGNLAFSDILVLFCSPPFL 109

DB 61 LQYFLIGLYTFVSLGLFGMGNLLILMAVMKKNQKTTVNFIGNLAFSDILVLFCSPPFL 120
 QY 110 TSVLLQWFMFGKVMCHIMPFLQCVSVLSTLILSTAIYRYHMKHPISNNLTANHGYEL 169
 DB 121 TSVLLQWFMFGKVMCHIMPFLQCVSVLSTLILSTAIYRYHMKHPISNNLTANHGYEL 180
 QY 170 IATVWTLGFAICSPPLPVFHSVLVELOTFGSALLSSRYLCVESWPSDVIAFTISLLVQ 229
 DB 181 IATVWTLGFAICSPPLPVFHSVLVELOTFGSALLSSRYLCVESWPSDVIAFTISLLVQ 240
 QY 230 YILPLVCLTVSHTSVCSISCGLSNKENLEBENMINLTLPSSKSGPGVKLSGSHKWSY 289
 DB 241 YILPLVCLTVSHTSVCSISCGLSNKENLEBENMINLTLPSSKSGPGVKLSGSHKWSY 300
 QY 290 SFTKHRRYKSKTACVLPAPERPSQENHSRTLPENFGSVRSQSSSKFIQVPTCFEI 349
 DB 301 SFIRKRRYKSKTACVLPAPAGSQEKLTVPENFGSVRSQSSSKFIQVPTCFEI 359
 QY 350 KPENSVDHELKRSVTRIKRSRSVFYRLTILILVFAVSWPLHLFHVTFDFNDNIS 409
 DB 360 KPESSDAQEMRVKRSLSLTKRSRSVFYRLTILILVFAVSWPLHLFHVTFDFNDNIS 419
 QY 410 NRHFKLIVYICHLGLGWSCLNPILYGLNNGIKADLVSLHCLHM 455
 DB 420 NRHFKLIVYICHLGLGWSCLNPILYGLNNGIKADLVSLHCLHM 465
 RESULT 8
 BAC32426 PRELIMINARY; PRT; 466 AA.
 ID BAC32426
 AC BAC32426;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
 DE library, clone:B230213K17 product:NEUROPEPTIDE Y RECEPTOR TYPE 5, full
 DE insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carrinci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carrinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RESULT 9
NY5R PIG

Query Match 85.0%; Score 2028; DB 1; Length 446;
 Best Local Similarity 85.4%; Pred. No. 6.4e-127;
 Matches 380; Conservative 34; Mismatches 31; Indels 0; Gaps 0;

QY 11 MDLEDEYNNKTLATENNNTAATNSDPVMDYKSSVDDLOQFLGLTYFVSLGFMGNL 70
 DB 1 MGSEIPDYNNKTLASENNIVATNSGFPVWEDYKSSVDDLOQFLGLTYFVSLGFMGNL 60
 QY 71 LILMALMKRNOKTTVNFILGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHIMPFL 130
 DB 61 LILMAVMKRNOKTTVNFILGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHIMPFL 120
 QY 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAICSPLPVFHSL 190
 DB 121 QCVTVLVSTLILISIAIVRYHMKHPVSNLTANHGYFLIATVTLGLAICSPLPVFHSL 180
 QY 191 VELOETFGSALSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 250
 DB 181 VELOESFGSAWSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRITSC 240
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYSPFKKHRRYSKKTACVLPAP 310
 DB 241 GLSSQSKLEENEMINLTLPKAKRSGPAKLSHHPKWTYSIRRRHRRYSKKTACVRPAP 300
 QY 311 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHELRKRSVTRIK 370
 DB 301 AGPALESREGRPPGVKSGVMSQSPPSNKFMPGVPTCFEVPKEENSVDVPMRVSRSIMRLR 360
 QY 371 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 430
 DB 361 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 420
 QY 431 NPILYGLNNGIKADLVSLIHLCHM 455
 DB 421 NPILYGLNNGIKADLVSLIHLCHV 445

RESULT 10

Q8QFM2 ID Q8QFM2 PRELIMINARY; PRT; 443 AA.
 AC Q8QFM2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Neuropeptide Y receptor Y5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Holmberg S.K.S.; Mikko S.; Boswell T.; Zoorob R.; Larhammar D.;
 RT "Pharmacological characterization of cloned chicken neuropeptide Y
 RT receptors Y1 and Y5."
 RL J. Neurochem. 0:0-0(2003).
 DR EMBL; AY040844; AAK83556.1; --
 DR GO; GO:0046021; C:integral to membrane; IEA.
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000393; NPY5_Receptor.
 DR InterPro; IPR000611; NPY5_Receptor.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01016; NREPTIDEYR.
 DR PRINTS; PR01012; NREPTIDEYR.
 DR PROSITE; PS0262; G.PROTEIN_RCEP_F1_2; 1.
 KW Neuropeptide; Receptor
 SQ SEQUENCE 443 AA; 50044 MW; EFE9FLA391CC092S CRC64;

Query Match

Best Local Similarity 68.3%; Score 1629.5; DB 2; Length 443;
 Matches 310; Conservative 51; Mismatches 77; Indels 5; Gaps 4;
 QY 11 MDLEDEYNNKTLATENNNTAATNSDPVMDYKSSVDDLOQFLGLTYFVSLGFMGNL 70
 DB 1 MDLGFQDYNNRT-PTKNTSATTKN--PSAWEDYKSSVDDIOYFLGLTYLISLAGFVGNL 57
 QY 71 LILMALMKRNOKTTVNFILGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHIMPFL 130
 DB 58 LVLTLAL-TRKQKQITINILGNLAFSDILVLFCSPPFTLTSVLLDQWFGKVMCHIMPFL 116
 QY 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAICSPLPVFHSL 190
 DB 117 QCVTVLVSTLILISIAIVRYHMKHPVSNLTANHGYFLIATVTLGFAICSPLPVFHSL 176
 QY 191 VELOETFGSALSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 250
 DB 177 VDLRKTNLNLEALENRLLCIESWPSDSYRIAFITISLLVQYILPLVCLTASHTSVCRSVGS 236
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYSPFKKHRRYSKKTACVLPAP 310
 DB 237 RUSKKEGKFOENEMINLTLPKSKAGTEAQPSSHTSWSICALYRKHHRRYSKKTSTVMPAI 296
 QY 311 ERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDVHE-LRVKRSVTRI 369
 DB 297 LRQQQADFRDLPETSGTEKSQLSSSKFIPGVPTCFEMKPEENTEIQDMITVSQSIIRI 356
 QY 370 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 429
 DB 357 KRSRSVFRVRLTLLIIVFAVSNMPLHFLHVDTDFNDNLISNHFHKLVCICHLGWSGCC 416
 QY 430 NPILYGLNNGIKADLVSLIHLCH 452
 DB 417 NPILYGLNNGIKADLVSLIHLCH 439

RESULT 11

073733 ID 073733 PRELIMINARY; PRT; 377 AA.
 AC 073733;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Neuropeptide Y/peptide Y receptor Ya.
 GN Names=NPYra; Synonyms=NPYRYA;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98068842; PubMed=9407007;
 RA Lundell I.; Berglund M.M.; Starback P.; Salaneck E.; Gehlert D.R.;
 RA Larhammar D.;
 RT "Cloning and characterization of a novel neuropeptide Y receptor
 RT subtype in the zebrafish."
 RL DNA Cell Biol. 16:1357-1363 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98096393; PubMed=9434780;
 RA Ringvall M.; Berglund M.M.; Larhammar D.;
 RT "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
 RT subtype in the zebrafish."
 RL Biochem. Biophys. Res. Commun. 241:749-755 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99337783;
 RA Starback P.; Lundell I.; Fredriksson R.; Berglund M.M.; Yan Y.L.;
 RA Wraath A.; Soderberg C.; Postlethwait J.H.; Larhammar D.;
 RT "Neuropeptide Y receptor subtype with unique properties cloned in the
 RT zebrafish: the zya receptor."

Brain Res. Mol. Brain Res. 70:242-252 (1999).
EMBL; AF037400; AAC41276.1; -.
ZFIN; ZDB-GENE-980526-393; npyrya.
GO: GO:016021; C:integral to membrane; IEA.
GO: GO:0004983; F:neuropeptide y receptor activity; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007218; F:neuropeptide signaling pathway; IEA.
InterPro: IPR000276; GPCR_Rhodopsn.
InterPro: IPR000351; NPY_receptor.
InterPro: IPR000611; NPY_receptor.
Pfam: PF00001; 7tm1; 1.
PRINTS; PR00237; GPCR_Rhodopsn.
PRINTS; PR01013; NRPEPTIDEYR.
PRINTS; PR01012; NRPEPTIDEYR.
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
Neuropeptide; Receptor.
SEQUENCE 377 AA; 42901 MW; .60862AD9C7BF5D0 CRC64;
Query Match 23.4%; Score 538; DB 2; Length 377;
Best Local Similarity 28.6%; Pred. No. 3.4e-29;
Matches 124; Conservative 68; Mismatches 136; Indels 106; Gaps 6;
QY 20 NKTATENTNATRNDRPVDYKSSVDDQLQYFLIGLYTFTVSLILGFMGNLLILMALMKK 79
DB 16 NSTLTHNQNSSLFLDVPW---QSSWTWLT--LVLCYCLVLILGLGNLLICIIMHQ 70
QY 80 NQKTTVNLGNLAPSDILVLPFCPTLTSVLLDQWFGKVMCHIMPFLLQCVSLVST 139
DB 71 RPPNVTSTLIANLSVSDILSVFCLPFTVTVVTLMDHIFGALLCLRLMPFVQCVSVTVSV 130
QY 140 LILISIAIVRYHMKHIPSNNLTANHGYFLIATVTLGFAICSPLEVPFHSVLVELQETFGS 199
DB 131 LSLVILAEHQLLHPSCKVSPQAVIANLTWLLACTVSLPFLAFHLLTSPYSLFP 190
QY 200 ALLSSRYLCVSPSDSVRIATISLLIQVILPLVCLTVSHTSVCSISGLSKENRL 259
DB 191 APLSQLQVLEVPQDQKLAITYTSLILFQVCCPLLMLLCYLR----- 235
QY 260 EENEMINLTLPSSKSGPQVLSGSHKWSYGFKKHRRYSKKTACVLPAPERPSQENHS 319
DB 236 -----FLRLQRERMLERQC-----SRNREHR 259
QY 320 RLLENFGSVRSQSSSKFIPGVPTCFEIKPENSDVHELVRKSVTRIKRSRVFYR 379
DB 260 RVN-----HSKRINVM 270
QY 380 LTLILVFAVSWMPLHLFHVWTFDNDNLISNRHFKLVYICICHLGMMSCCLNPLYLGFNL 439
DB 271 LATLVAFVAVCMPLNAPVNVADQCVLPVCNHNLLFSLCHLLANSSTCVNPLYLGFNL 330
QY 440 NGKADLVSLI-HC 452
DB 331 SNFRKDVASVVLHC 344
RESULT 12
Q6Y6A4 PRELIMINARY; PRT; 348 AA.
ID Q6Y6A4
AC Q6Y6A4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE NPY receptor Y1 (Fragment).
OS Squalus acanthias (Spiny dogfish).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hynostomales; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OC NCBI_TaxID=7797;
RN [1]
RP MEDLINE=22763539; PubMed=12777532;
SEQUENCE FROM N.A.
RA Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
RT "Three neuropeptide y receptor genes in the spiny dogfish, Squalus
acanthias, support en bloc duplications in early vertebrate
evolution.";
RL Mol. Biol. Evol. 20:1271-1280 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Salaneck E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY177273; AAO62565.1; -.
DR EMBL; AY177272; AAO62565.1; JOINED.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000351; NPY_receptor.
DR InterPro; IPR000611; NPY_receptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01013; NRPEPTIDEYR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 348
SQ SEQUENCE 348 AA; 40738 MW; 817D35C3DAFD90F CRC64;
Query Match 22.1%; Score 527; DB 2; Length 348;
Best Local Similarity 25.7%; Pred. No. 3.6e-27;
Matches 115; Conservative 79; Mismatches 122; Indels 132; Gaps 7;
QY 5 SKQDYNMDELDEYVNYKTLATENTNATRNDRPVDYKSSVDDQLQYFLIGLYTFTVSL 64
DB 19 SERNFTLD-NYDQCVSQT-----MIPTLALIVSAILIL 51
QY 65 GPMGNLLILMALMKRKNOKTIVNFIQNLAFSDILVLPFCPTLTSVLLDQWFGKVMC 124
DB 52 GYSGNLLIITIMKREKHNVTNLIYNLSVSDILISWCLPFTLVYTFMDHIFGAMC 111
QY 125 HIMPFLQCVSLVSTLILISIAIVRYHMKHIPSNNLTANHGYFLIATVTLGFAICSP 184
DB 112 KLSNMIQICISITVIFSLVLAVERHQLINPQGRPNKKNHAYLSIVTWTLALLTSLPP 171
QY 185 PVFHSVLVQLQTFG-SALLSSRYLCVSPSDSVRIATISLLIQVILPLVCLTVSHTS 243
DB 172 LLEFNLTDQEFHHGYSTEFAGKYNCLBQWSETORLVYTTCLLMQVAFPLCFICYFK 231
QY 244 VCRSISCLSKENKLEENEMINLTLPSSKSGPQVLSGSHKWSYGFKKHRRYSKKT 303
DB 232 I-----YLRNRNNTM-- 243
QY 304 ACVLPAPERPSQENHSRLPENFGSVRSQSSSKFIPGVPTCFEIKPENSDVHELVRK 363
DB 244 -----DKREEN-----KYRADEN----- 257
QY 364 RSVTRIKRSRVFYRLTILVFAVSWMPLHLFHVWTFDNDNLISNRHFKLVYICICHL 423
DB 258 -----RRINMLISIVFAICWLPLNTFNAVFDWNVEYVNNCHNLVFSICHLT 307
QY 424 GMMSCCLNPLYLGFNLGIRADLVSLIH 451
DB 308 AMLSTCTNPIFYGFENKFNQFQDLSILH 335
RESULT 13
AAO62565 PRELIMINARY; PRT; 348 AA.
ID AAO62565
AC AAO62565
DT 25-MAR-2004 (TRENBLrel. 27, Created)
DT 25-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE NPY receptor Y1 (Fragment).
OS Squalus acanthias (Spiny dogfish).
SEQUENCE FROM N.A.
RP MEDLINE=22763539; PubMed=12777532;

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22763539; PubMed=12777532;
RA   Salanek E., Ardell D.H., Larson E.T., Larhammar D.;
RT   "Three Neuroptide Y Receptor Genes in the Spiny Dogfish, Squalus
RT   acanthias, Support en Bloc Duplications in Early Vertebrate
RT   Evolution.";
RL   Mol. Biol. Evol. 20:1271-1280(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Salanek E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC   -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY177271; AAO62564.1; -
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR000276; GPCR_Rhodopsin.
DR   InterPro; IPR000986; Neuroy6_receptor.
DR   InterPro; IPR000351; NPY1_receptor.
DR   InterPro; IPR000611; NPY2_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCR_Rhodopsin.
DR   PRINTS; PR01013; NRPEPTIDEYR.
DR   PRINTS; PR01017; NRPEPTIDEYR.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE 348 AA; 40738 MW; 817D35C53DAFD90F CRC64;

Query Match      22.1%; Score 527; DB 2; Length 348;
Best Local Similarity 25.7%; Pred. No. 3.6e-27;
Matches 115; Conservative 79; Mismatches 122; Indels 132; Gaps 7;

QY   5 SKQDYNMDELDYVYKTLATNTATRNDDPVDYKSSVDLQVFLGLTYFVSL 64
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   65 GFMGNLLIIMALKRNQKTTNFIIGNLAFSDILVLFQSPFTLTVLLDQWFGKVMC 124
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   125 HMFPLQCVSVLSTLIISIAVRYHMKHPISNNLTANHGYELIATVMTLGAICSP 184
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   185 PVFSLVLEQTFG-SALLSRYLCVSWPSDSYRIAFITSLILVQYILPLVCLTVSHTS 243
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   172 LFLNLTDEQHHGYSTEFAGKQWCLQWSESTQRLVTTCLLQWPAFLCFICYFK 231
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   244 VCRISGLSNKENLEENEMINLTLPKSKSGQVKSLSGSHKWSYFIKKHRRYSKKT 303
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   304 ACVLPAPEPSQENHSLRILPENFQSVRSQSSSKKFTPGVPTCFEIKPENSDVHLRVK 363
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   364 RSVTRIKRSRVFYRITLILVFAVSWMPHLFHVVTDFNDNLINRHPKLVYCICHL 423
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   424 GMSCCNLPILYGLFANGIKADLVSLIH 451
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   308 AMLSTCTNPIFYGLNKNFQDLRSILH 335
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
QY6AS PRELIMINARY; PRT; 373 AA.
AC QY6AS, 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE NPY receptor Y6.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hyposqualae; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.

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RX   MEDLINE=22763539; PubMed=12777532;
RA   Salanek E., Ardell D.H., Larson E.T., Larhammar D.;
RT   "Three neuroptide y receptor genes in the spiny dogfish, Squalus
RT   acanthias, support en bloc duplications in early vertebrate
RT   evolution.";
RL   Mol. Biol. Evol. 20:1271-1280(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Salanek E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC   -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY177271; AAO62564.1; -
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR000276; GPCR_Rhodopsin.
DR   InterPro; IPR000986; Neuroy6_receptor.
DR   InterPro; IPR000351; NPY1_receptor.
DR   InterPro; IPR000611; NPY2_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCR_Rhodopsin.
DR   PRINTS; PR01013; NRPEPTIDEYR.
DR   PRINTS; PR01017; NRPEPTIDEYR.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE 373 AA; 42961 MW; 652E44A1F11DB9F5 CRC64;

Query Match      21.9%; Score 522.5; DB 2; Length 373;
Best Local Similarity 26.4%; Pred. No. 7.8e-27;
Matches 117; Conservative 71; Mismatches 134; Indels 121; Gaps 7;

QY   19 YNKLATENTNTAATRNDDPVDYKSS--SVDDLQVFLGLTYFVSLGLFGMNLILMAL 76
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   77 MKRNQKTTNFIIGNLAFSDILVLFQSPFTLTVLLDQWFGKVMCHIMPFQCVSVL 136
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   63 KQKENHNVNTLIANLSVSDVFCWMCIPETIVTLMYVIFGDMCKANSFIQCVSVT 122
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   137 VETLILSIAIVRYHMKHPISNNLTANHGYELIATVMTLGAICSPPLVPHSLVLEQET 196
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   123 VSIFSLVLIATERHQLIIVNPRGWKPSVSHACWGLVLIWFVSLIISFFPIILHLLTD--EP 180
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   197 F-----GSALLSRYLCVSWPSDSYRIAFITSLILVQYILPLVCLTVSHTS--VCRSIS 249
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   181 FRNVSSHSEFYKDFKVCIEIWFSEADRLVFTTCLLIQYPAFLCFIFVCYLKIFVCLKKR 240
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   250 CGLSNKENLEENEMINLTLPKSKSGQVKSLSGSHKWSYFIKKHRRYSKKTACVLP 309
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY   310 PERPSQENHSLRILPENFQSVRSQSSSKKFTPGVPTCFEIKPENSDVHLRVKRSVTRI 369
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   247 ---MRENESRV-----
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Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   255 -NESKRNIMLASIVFAFTVCLWELNINNVVDFWDMHEALMKNCHYNLVFTICHTAMISTC 313
Db   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY   430 LNPILYGLNNGIKADLVSLIH 452
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QY   314 INPIFYGLNKNFQDLNMLIH 336
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RESULT 15
AAO62564 PRELIMINARY; PRT; 373 AA.
ID AAO62564
AC AAO62564;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NPY receptor Y6.

```

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OS Squalus acanthias (Spiny dogfish)..
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22763539; PubMed=12777532;
RA Salanek E., Ardell D.H., Larson E.T., Larhammar D.;
RT "Three Neuropeptide Y Receptor genes in the Spiny Dogfish, Squalus
RT acanthias, Support en Bloc Duplications in Early Vertebrate
RT Evolution.";
RL Mol. Biol. Evol. 20:1271-1280(2003).
[2]
RN SEQUENCE FROM N.A.
RP Salanek E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL; AY17271; AAC62564.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42961 MW; 652E44A1F11DE9F5 CRC64;

Query Match 21.9%; Score 522.5; DB 2; Length 373;
Best Local Similarity 26.4%; Pred. No. 7.8e-27;
Matches 11; Conservative 71; Mismatches 134; Indels 121; Gaps 3;

QY 19 YNKTLATENNNTAATRNSDFFPVWDDYKS--SVDDIQYFLIGLYTFVSLGLGFMGNLLIMAL 76
DB 6 YNHSV--NISEVTHDGRQPFADFQSCASSPVNFFLLILAYGTVTVGLFGNLCIFII 62

QY 77 MKXRNQKTVNFLGNLAFSDILVVLPCSPETLSVLLDQWFKGMCHIMPELQCVSVL 136
DB 63 KRQENHNVTNILLANLVSVDVFCVCMCIPETIVTLLMDYWFQDMCKANSFIQCVSVT 122

QY 137 VSTLILISIAIVRYHMIKHPISNNLTANHGYFLIATVMTLGFACISPLVPFHSILVLEQET 196
DB 123 VSPESLVIIAIEHQILVNPGRKPSVSHACGWIVLWFSIIISFPFIIPHLLTD--EP 180

QY 197 F-----GSALLSSRYLQVESWPSDSYRIAFITISILLVQYIILPLVCLTYSHTS--VCRSIS 249
DB 181 FRNVSSHSEFYKDFKVFCTEIIWPSADRLVFTTCLILQYFAPLQCFIFVCYLIKIFVCLKKR 240

QY 250 CGLSNKENRLNEENMINLTLHPKKSGQVKLSGSHKWSYSFIKKHRRRYSKKTACVLPA 309
DB 241 NGMADK----- 246

QY 310 PERPSQENHSRILPENFGSVRSQSSSSKFIPGVPTCEIKPEENSVDVHELVRKSVTRI 369
DB 247 ---MRENSRV----- 254

QY 370 KKRERSVYRLLTILLVFAVSWMPHLPHVYVTFDNDNLISNREHFKLVYICILHGMWSSC 429
DB 255 -NEKRIINMLASIVYAVTQVCLVPLNINNVVFDWNEALMCHNYLVFTLCHLTANI STC 313

QY 430 LNPILYGFNNIGIKADLVSLIHC 452
DB 314 INPIYGFNNKFNQKDLNLIHC 336

Search completed: October 21, 2004, 12:13:17
Job time : 193 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2004, 12:01:30 ; Search time 39 seconds
(without alignments)
773.710 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385
Sequence: 1 MSFYSKQYNDMDLEDEYNN.....GFLNNGIKADLVSLHCLHM 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents_AA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2385	100.0	455	1	US-08-349-025-4
2	2385	100.0	455	2	US-08-566-096A-4
3	2385	100.0	455	2	US-08-668-650B-4
4	2385	100.0	455	3	US-09-200-673-4
5	2385	100.0	455	4	US-09-194-895-4
6	2385	100.0	455	4	US-10-013-846-7
7	2385	100.0	455	4	US-09-447-907-4
8	2385	100.0	455	5	PCT-US95-15646-4
9	2330	97.7	445	2	US-08-630-118A-6
10	2330	97.7	445	2	US-08-838-399-6
11	2330	97.7	445	2	US-09-003-139-21
12	2330	97.7	445	3	US-09-233-839-6
13	2330	97.7	445	3	US-09-327-035-6
14	2330	97.7	445	4	US-09-065-027-2
15	2330	97.7	445	4	US-09-708-392-13
16	2326	97.5	445	4	US-09-065-027-4
17	2318	97.2	445	3	US-09-040-958-2
18	2318	97.2	445	3	US-09-040-958-4
19	2266	95.0	445	2	US-09-003-139-2
20	2262	94.8	456	2	US-08-668-650B-14
21	2262	94.8	456	4	US-09-194-895-14
22	2262	94.8	456	4	US-09-447-907-14
23	2084.5	87.4	456	1	US-08-349-025-2
24	2084.5	87.4	456	2	US-08-566-096A-2
25	2084.5	87.4	456	2	US-08-668-650B-2
26	2084.5	87.4	456	3	US-09-200-673-2
27	2084.5	87.4	456	4	US-09-194-895-2

28 2084.5 87.4 456 4 US-09-447-907-2 Sequence 2, Appli
29 2084.5 87.4 456 5 PCT-US95-15646-2 Sequence 2, Appli
30 2074.5 87.0 445 2 US-08-630-118A-4 Sequence 4, Appli
31 2074.5 87.0 445 2 US-08-838-399-4 Sequence 4, Appli
32 2074.5 87.0 445 2 US-09-003-139-23 Sequence 23, Appli
33 2074.5 87.0 445 3 US-09-233-839-4 Sequence 4, Appli
34 2074.5 87.0 445 3 US-09-327-035-4 Sequence 4, Appli
35 2074 87.0 466 4 US-09-065-027-8 Sequence 8, Appli
36 2072.5 86.9 445 4 US-09-065-027-6 Sequence 6, Appli
37 2067.5 86.7 445 2 US-08-630-118A-2 Sequence 2, Appli
38 2067.5 86.7 445 2 US-08-838-399-2 Sequence 2, Appli
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40 2067.5 86.7 445 3 US-09-327-035-2 Sequence 2, Appli
41 1671 70.1 334 2 US-08-566-096A-6 Sequence 6, Appli
42 1671 70.1 334 3 US-08-668-650B-6 Sequence 6, Appli
43 1671 70.1 334 3 US-09-200-673-6 Sequence 6, Appli
44 1671 70.1 334 4 US-09-194-895-6 Sequence 6, Appli
45 1671 70.1 334 4 US-09-447-907-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-349-025-4
; Sequence 4, Application US/08349025
; Patent No. 5602024
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Walker, Mary W.
; APPLICANT: Wainshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
; TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/349,025
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1795/46166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-025-4

Query Match 100.0%; Score 2385; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.3e-180;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSFYSKQYNDMDLEDEYNNATATRNDFPVNDYKSSVDDI-QYFLIGLYTF 60
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Db 1 MSFYSQDYNMDELDEYNNKTATNTAATNSDFPVDYKSSVDDLOFLGLYTF 60
 QY 61 VSLGPMGNLLIIMALKKRNQKTTNFIIGNLAFSDILWLFCSPFTLTSLVLLDQWFG 120
 Db 61 VSLGPMGNLLIIMALKKRNQKTTNFIIGNLAFSDILWLFCSPFTLTSLVLLDQWFG 120
 QY 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180
 Db 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 QY 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKSGLSHKWSYFIKHHRRYS 300
 Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKSGLSHKWSYFIKHHRRYS 300
 QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360
 Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 Db 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 QY 421 HLLGWMSCCLNPILYGLFNNGIKADLVSLIHCLHM 455
 Db 421 HLLGWMSCCLNPILYGLFNNGIKADLVSLIHCLHM 455

RESULT 2

US-08-566-096A-4
 ; Sequence 4, Application US/08566096A
 ; Patent No. 5968819
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe P.G.
 ; APPLICANT: Walker, Mary W.
 ; APPLICANT: Branchek, Theresa
 ; APPLICANT: Weinshank, Richard L.
 ; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR.
 ; TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC
 ; TITLE OF INVENTION: NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (YS) AND USES THEREOF
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/566,096A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 1795/46166-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 455 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-566-096A-4

Query Match 100.0%; Score 2385; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred No. 5,3e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180
 Db 121 KVMCHIMPFLQCVSVLVSTLIIISIAIVRYHMKHPIISNNLTANHGYFLIATVWTLGFAI 180
 QY 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 Db 181 CSPLPVHSLVLOETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 QY 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKSGLSHKWSYFIKHHRRYS 300
 Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPSPKSGPQVKSGLSHKWSYFIKHHRRYS 300
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 Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPOVPTCFEIKPEENSVDVHEL 360
 QY 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 Db 361 RVKRSVTRIKKRSRVFVRLTILILVFAVSNMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 QY 421 HLLGWMSCCLNPILYGLFNNGIKADLVSLIHCLHM 455
 Db 421 HLLGWMSCCLNPILYGLFNNGIKADLVSLIHCLHM 455

RESULT 3

US-08-668-650B-4
 ; Sequence 4, Application US/08668650B
 ; Patent No. 5989920
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe P.G.
 ; APPLICANT: Waker, Mary W.
 ; APPLICANT: Branchek, Theresa
 ; APPLICANT: Weinshank, Richard L.
 ; TITLE OF INVENTION: Methods of Modifying Feeding Behavior,
 ; TITLE OF INVENTION: Compounds Useful in Such Methods, And DNA Encoding a
 ; TITLE OF INVENTION: Hypothalamic Atypical Neuropeptide Y/Peptide YY Receptor
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/668,650B
 ; FILING DATE: 04-JUN-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White Esq., John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 1795/46166C

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 455 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-668-650B-4

Query Match 100.0%; Score 2385; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 5.3e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYKODYNMDLELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60
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 DB 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120

QY 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180
 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180

QY 181 CSPLPVFHSLVQLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 DB 181 CSPLPVFHSLVQLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300
 DB 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300

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 DB 421 HLLGMSCCLNPILYGLFNGIKADLVSLIHCLHM 455

RESULT 4
 US-09-200-673-4
 Sequence 4, Application US/09200673A
 Patent No. 6316203

GENERAL INFORMATION:
 APPLICANT: Gerald, Christophe P.G.
 APPLICANT: Weinstank, Richard L.
 APPLICANT: Walker, Mary W.
 APPLICANT: Branchek, Theresa
 TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
 TITLE OF INVENTION: In Such Methods, and DNA Encoding A Hypothalamic
 TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)
 FILE REFERENCE: 46166-RZ/JPW
 CURRENT APPLICATION NUMBER: US/09/200,673A
 PRIOR FILING DATE: 1998-11-25
 EARLIER APPLICATION NUMBER: 08/566,096
 EARLIER FILING DATE: 1995-12-01
 EARLIER APPLICATION NUMBER: 08/349,025
 EARLIER FILING DATE: 1994-12-02
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 455
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-200-673-4

Query Match 100.0%; Score 2385; DB 3; Length 455;
 Best Local Similarity 100.0%; Pred. No. 5.3e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYKODYNMDLELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60
 DB 1 MSFYKODYNMDLELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120
 DB 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120

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 DB 121 KVMCHIMPFLQCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVWTLGFAI 180

QY 181 CSPLPVFHSLVQLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
 DB 181 CSPLPVFHSLVQLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240

QY 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300
 DB 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKKHRRYS 300

QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360
 DB 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSVDHEL 360

QY 361 RVKRSVTRIKKRSRVFRLITILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
 DB 361 RVKRSVTRIKKRSRVFRLITILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMSCCLNPILYGLFNGIKADLVSLIHCLHM 455
 DB 421 HLLGMSCCLNPILYGLFNGIKADLVSLIHCLHM 455

RESULT 5

US-09-194-895-4
 Sequence 4, Application US/09194895
 Patent No. 6531287

GENERAL INFORMATION:
 APPLICANT: Gerald, Christophe P.G.
 APPLICANT: Weinstank, Richard L.
 APPLICANT: Walker, Mary M
 APPLICANT: Branchek, Theresa
 TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
 TITLE OF INVENTION: In Such Methods and DNA Encoding A Hypothalamic
 TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)
 FILE REFERENCE: 1795-46166-D-PCT-US/JPW/BJA
 CURRENT APPLICATION NUMBER: US/09/194,895
 PRIOR FILING DATE: 1999-09-27
 PRIOR APPLICATION NUMBER: PCT/US97/09504
 PRIOR FILING DATE: 1997-06-04
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 455
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-194-895-4

Query Match 100.0%; Score 2385; DB 4; Length 455;
 Best Local Similarity 100.0%; Pred. No. 5.3e-180;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYKODYNMDLELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60
 DB 1 MSFYKODYNMDLELDEYNNKTLATENTTAATRNSDFFVWDDYKSSVDDQLQYFLIGLYTF 60

QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSVLLDQWFG 120

```

Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQWFG 120
Qy 121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Db 121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Qy 181 CSPLPVHSLVLEQTFGSGALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db 181 CSPLPVHSLVLEQTFGSGALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Qy 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIKPVPTCFEIKPEENSVDVHEL 360
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIKPVPTCFEIKPEENSVDVHEL 360
Qy 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Qy 421 HLLGWMSCCLNPILYGLFNGGKADLVSLIHCLHM 455
Db 421 HLLGWMSCCLNPILYGLFNGGKADLVSLIHCLHM 455

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RESULT 6

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US-10-013-846-7
; Sequence 7, Application US/10013846
; Patent No. 6566367
; GENERAL INFORMATION:
; APPLICANT: Bakhtavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Briemann, Harry L
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Mariya
; TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
; FILE OF INVENTION: 3H-spiroisobenzofuran-1,4'-piperidines
; FILE REFERENCE: N00.2001
; CURRENT APPLICATION NUMBER: US/10/013,846
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 455
; TYPE: PRT
; ORGANISM: hom sapiens
US-10-013-846-7

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Query Match 100.0%; Score 2385; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.3e-180;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFYSKQDYNMDELDEYNNKTLATENNNTAATRSDFPVDYKSSVDDIQLYFLIGLYTF 60
Db 1 MSFYSKQDYNMDELDEYNNKTLATENNNTAATRSDFPVDYKSSVDDIQLYFLIGLYTF 60
Qy 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQWFG 120
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQWFG 120
Qy 121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Db 121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180

```

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Qy 181 CSPLPVHSLVLEQTFGSGALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db 181 CSPLPVHSLVLEQTFGSGALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Qy 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIKPVPTCFEIKPEENSVDVHEL 360
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIKPVPTCFEIKPEENSVDVHEL 360
Qy 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Qy 421 HLLGWMSCCLNPILYGLFNGGKADLVSLIHCLHM 455
Db 421 HLLGWMSCCLNPILYGLFNGGKADLVSLIHCLHM 455

```

RESULT 7

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US-09-447-907-4
; Sequence 4, Application US/09447907
; Patent No. 6645774
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Weinshank, Richard L
; APPLICANT: Walker, Mary W
; APPLICANT: Brancheck, Theresa
; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful in Such Me
; FILE OF INVENTION: and DNA Encoding A Hypothalamic Atypical Neuropeptide Y/Peptide
; FILE REFERENCE: 1795-46166CA
; CURRENT APPLICATION NUMBER: US/09/447,907
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 08/668,650
; PRIOR FILING DATE: 1996-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Y5 cDNA clone
US-09-447-907-4

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Query Match 100.0%; Score 2385; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.3e-180;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFYSKQDYNMDELDEYNNKTLATENNNTAATRSDFPVDYKSSVDDIQLYFLIGLYTF 60
Db 1 MSFYSKQDYNMDELDEYNNKTLATENNNTAATRSDFPVDYKSSVDDIQLYFLIGLYTF 60
Qy 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQWFG 120
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVDQWFG 120
Qy 121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Db 121 KVMCHIMPLOQCVSLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGF 180
Qy 181 CSPLPVHSLVLEQTFGSGALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db 181 CSPLPVHSLVLEQTFGSGALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Qy 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Db 241 HTSVCRSISCGLSNKENLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Qy 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIKPVPTCFEIKPEENSVDVHEL 360

```

Db

301

KTACVLPAPERSENHRSILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL

360

Qy

361

RVKRSVTRIKRGRSVFYRLTILILVFAVSWMPHLHFVHTDNDNLISNRHFKLVYCIC

420

Db

361

RVKRSVTRIKRGRSVFYRLTILILVFAVSWMPHLHFVHTDNDNLISNRHFKLVYCIC

420

Qy

421

HLGWMSCCLNPILYGFLLNGIKADLVSLIHCLHM

455

Db

421

HLGWMSCCLNPILYGFLLNGIKADLVSLIHCLHM

455

RESULT 8

PCT-US95-15646-4

; Sequence 4, Application PC/TUS9515646

; GENERAL INFORMATION:

; APPLICANT: Syntactic Pharmaceutical Corporation

; TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, COMPOUNDS

; TITLE OF INVENTION: USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC ATYPIC

; TITLE OF INVENTION: Y/PEPTIDE YY RECEPTOR (YS) AND USES THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15646

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 1795/46166-A-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 456 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US95-15646-4

Query Match

Best Local Similarity

Matches

455;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

1

MSFYKQDYNMDELDYYNKTATNTAATRNDDYKSSVDDLOVFLGLTYF

60

Db

1

MSFYKQDYNMDELDYYNKTATNTAATRNDDYKSSVDDLOVFLGLTYF

60

Qy

61

VLLGFMGNLLIIMALKKRNKQTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFG

120

Db

61

VLLGFMGNLLIIMALKKRNKQTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFG

120

Qy

121

KVCHIMPFLQCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFIATVTLGAI

180

Db

121

KVCHIMPFLQCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFIATVTLGAI

180

Qy

181

CSPLPVFHSVLVEIQETFGSALLSSRYLCVESPSSSYRAFTISLLLVQYILPLVCLTVS

240

Db

181

CSPLPVFHSVLVEIQETFGSALLSSRYLCVESPSSSYRAFTISLLLVQYILPLVCLTVS

240

Qy

241

HTSVCRSISGLSNKENRLEENEMINLTLPKSKGPGVKLSGSHKWSYFIKKHRRYS

300

Db

241

HTSVCRSISGLSNKENRLEENEMINLTLPKSKGPGVKLSGSHKWSYFIKKHRRYS

300

Qy

301

KTACVLPAPERSENHRSILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL

360

Db

301

KTACVLPAPERSENHRSILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL

360

Qy

361

RVKRSVTRIKRGRSVFYRLTILILVFAVSWMPHLHFVHTDNDNLISNRHFKLVYCIC

420

Db

361

RVKRSVTRIKRGRSVFYRLTILILVFAVSWMPHLHFVHTDNDNLISNRHFKLVYCIC

420

Qy

421

HLGWMSCCLNPILYGFLLNGIKADLVSLIHCLHM

455

Db

421

HLGWMSCCLNPILYGFLLNGIKADLVSLIHCLHM

455

RESULT 9

US-08-630-118A-5

; Sequence 6, Application US/08630118A

; Patent No. 5919901

; GENERAL INFORMATION:

; APPLICANT: Hu Ph.D., Yinghe

; APPLICANT: McCaleb Ph.D., Michael L.

; APPLICANT: Bloomquist Ph.D., Brian T.

; APPLICANT: Flores-Riveros Ph.D., Jaime R.

; APPLICANT: Cornfield Ph.D., Linda J.

; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

; TITLE OF INVENTION: Sequences

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive, 32nd Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,118A

; FILING DATE: April 8, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Greenfield Ph.D., Michael S.

; REGISTRATION NUMBER: 37,142

; REFERENCE/DOCKET NUMBER: 96,149/WH 405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312)715-1000

; TELEFAX: (312)715-1234

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-630-118A-6

Query Match

Best Local Similarity

Matches

445;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

11

MDLEDDYYNKTATNTAATRNDDYKSSVDDLOVFLGLTYFVSLIGFNGNL

70

Db

1

MDLEDDYYNKTATNTAATRNDDYKSSVDDLOVFLGLTYFVSLIGFNGNL

60

Qy

71

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130

Db

61

LILMALKKRNKQTTVNFILGNLAFSDILVLFCSPTLTSVLLDQWFGKWMCHIMPFL

120

Qy

131

QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFIATVTLGAI

190

Db

131

QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFIATVTLGAI

190

Db 121 QCVSVLSTLILISIAIVRYHMKHPISSNNLTANHGYPFLIAVTWLTGFAICSPFVPHSL 180
QY 191 VELOETFGSALLSRVLCVESWPSDSYRIAFTAFISILLVQYIILPLVCLTVSHTSVCRSISC 250
Db 181 VELOETFGSALLSRVLCVESWPSDSYRIAFTAFISILLVQYIILPLVCLTVSHTSVCRSISC 240
QY 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYSPFKKHRRYKSKTACVLPAP 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYSPFKKHRRYKSKTACVLPAP 300
QY 311 ERPSQENHSHRILPENFGSVRSQSSSKKIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
Db 301 ERPSQENHSHRILPENFGSVRSQSSSKKIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360
QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 430
Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 420
QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455
Db 421 NPILYGLFNNGIKADLVSLIHCLHM 445

RESULT 10

US-08-838-399-6
; Sequence 6, Application US/08038399
; Patent No. 5965392
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCaleb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838.399
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-399-6

Query Match 97.7%; Score 2330; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDLELDYYNKTATENTNATNSDPFWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL 60
QY 71 LILMALMKKNQKTTNVNFLIGNLAFSDILVVLFCSPFTLTSLVLDQWFMGKVMCHIMPFL 130
Db 61 LILMALMKKNQKTTNVNFLIGNLAFSDILVVLFCSPFTLTSLVLDQWFMGKVMCHIMPFL 120
QY 131 QCVSVLSTLILISIAIVRYHMKHPISSNNLTANHGYPFLIAVTWLTGFAICSPFVPHSL 190
Db 121 QCVSVLSTLILISIAIVRYHMKHPISSNNLTANHGYPFLIAVTWLTGFAICSPFVPHSL 180
QY 191 VELOETFGSALLSRVLCVESWPSDSYRIAFTAFISILLVQYIILPLVCLTVSHTSVCRSISC 250
Db 181 VELOETFGSALLSRVLCVESWPSDSYRIAFTAFISILLVQYIILPLVCLTVSHTSVCRSISC 240
QY 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYSPFKKHRRYKSKTACVLPAP 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYSPFKKHRRYKSKTACVLPAP 300
QY 311 ERPSQENHSHRILPENFGSVRSQSSSKKIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
Db 301 ERPSQENHSHRILPENFGSVRSQSSSKKIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360
QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 430
Db 361 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 420
QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455
Db 421 NPILYGLFNNGIKADLVSLIHCLHM 445

RESULT 11

US-09-003-199-21
; Sequence 21, Application US/09003199
; Patent No. 5985616
; GENERAL INFORMATION:
; APPLICANT: Parker, Eric M
; APPLICANT: Strader, Catherine D
; APPLICANT: Rudinski, Mark S
; TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: NJ
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,199
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thampoe, Immac J.
; REGISTRATION NUMBER: 36,322
; REFERENCE/DOCKET NUMBER: CN0775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-5061
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-003-199-21

QY 11 MDLELDYYNKTATENTNATNSDPFWDDYKSSVDDLQYFLIGLYTFVSLGFMGNL 70

Query Match 97.7%; Score 2330; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 MDLEDEYNNKTLATENTNTAATNSDPVWDYKSSVDDLOVFLGLGLYTFVSLGFMGNL 70
1 MDLEDEYNNKTLATENTNTAATNSDPVWDYKSSVDDLOVFLGLGLYTFVSLGFMGNL 60

71 LILMALMKRNKNTTNVFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKVMCHIMPFL 130
61 LILMALMKRNKNTTNVFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKVMCHIMPFL 120

131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFLIATVTLGFAICSLPVFHS 190
121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFLIATVTLGFAICSLPVFHS 180

191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQVILPLVCLTVSHTSVCRSISC 250
181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQVILPLVCLTVSHTSVCRSISC 240

251 GLSNKENRLEENEMINLTLPKSKGQVQLSGSHKWSYFIKHHRRYSKKTACVLPAP 310
241 GLSNKENRLEENEMINLTLPKSKGQVQLSGSHKWSYFIKHHRRYSKKTACVLPAP 300

311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVTCTFEIKPEENSDVHELVRKSVTRIK 370
301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVTCTFEIKPEENSDVHELVRKSVTRIK 360

371 KRERSVVFRLTILILVFAVSWMPHLHFVVTDFNDNLISNRHFKLVYCIHLLGMMSCCL 430
361 KRERSVVFRLTILILVFAVSWMPHLHFVVTDFNDNLISNRHFKLVYCIHLLGMMSCCL 420

431 NPILYGFLNNGIKADLVSLIHCLHM 455
421 NPILYGFLNNGIKADLVSLIHCLHM 445

RESULT 12
US-09-235-839-6
Sequence 6, Application US/09235839
Patent No. 6207799

GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
APPLICANT: Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.

TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,839
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/630,118
FILING DATE: April 8, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D. Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 96,149-C

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-235-839-6

Query Match 97.7%; Score 2330; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 MDLEDEYNNKTLATENTNTAATNSDPVWDYKSSVDDLOVFLGLGLYTFVSLGFMGNL 70
1 MDLEDEYNNKTLATENTNTAATNSDPVWDYKSSVDDLOVFLGLGLYTFVSLGFMGNL 60

71 LILMALMKRNKNTTNVFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKVMCHIMPFL 130
61 LILMALMKRNKNTTNVFLGNLAFSDILVLFCSPTLTSVLLDQWFMGKVMCHIMPFL 120

131 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFLIATVTLGFAICSLPVFHS 190
121 QCVSVLVSTLILISIAIVRYHMKIPISNNLTANHGYPFLIATVTLGFAICSLPVFHS 180

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431 NPILYGFLNNGIKADLVSLIHCLHM 455
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RESULT 13
US-09-327-035-6
Sequence 6, Application US/09327035
Patent No. 6368824

GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
APPLICANT: Michael L.
APPLICANT: Bloomquist Ph.D., Brian T.
APPLICANT: Flores-Riveros Ph.D., Jaime R.
APPLICANT: Cornfield Ph.D., Linda J.

TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/327,035
/ FILING DATE: 07-Jun-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/838,399
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greenfield Ph.D., Michael S.
/ REGISTRATION NUMBER: 37,147
/ REFERENCE/DOCKET NUMBER: 96,149/WH 405
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312)715-1000
/ TELEFAX: (312)715-1234
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 445 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-327-035-6

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Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-065-027-2
Sequence 2, Application US/09065027
Patent No. 6528303
GENERAL INFORMATION:
APPLICANT: Heizog, H.
TITLE OF INVENTION: NEUROPEPTIDE Y-Y5 RECEPTOR
FILE REFERENCE: 273402001800
CURRENT APPLICATION NUMBER: US/09/065,027
CURRENT FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT/AU96/00706
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 8
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/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 445
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-065-027-2

Query Match          97.7%; Score 2330; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.1e-175;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 421 NPILYGLFNNGIKADLVSLIHCLHM 445

RESULT 15
US-09-708-392-13
Sequence 13, Application US/09708392
Patent No. 6734186
GENERAL INFORMATION:
APPLICANT: Pfizer Inc
APPLICANT: Pfizer Limited
APPLICANT: Wayman, Chris
APPLICANT: Naw, G
TITLE OF INVENTION: Pharmaceutical
FILE REFERENCE: PC10343AAKM
CURRENT APPLICATION NUMBER: US/09/708,392
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: GB 99266437.6
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: GB 0004021.2
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 0013001.3
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 0016563.9
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: GB 0017141.3
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/175,161
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/192,962
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/217,479
PRIOR FILING DATE: 2000-07-11
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Fri Oct 22 09:43:51 2004

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; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/221,093
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; TYPE: PRT
; LENGTH: 445
; ORGANISM: Homo sapiens
; US-09-708-392-13

Query Match      97.7%; Score 2330; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.le-175; Indels 0; Gaps 0;
Matches 445; Conservative 0; Mismatches 0;

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Search completed: October 21, 2004, 12:14:48
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2004, 12:07:45 ; Search time 129 Seconds

(without alignments)
1141.939 Million cell updates/sec

Title: US-09-771-956-13

Perfect score: 2385

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Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2385	100.0	455	14	US-10-013-846-7
4	2385	100.0	455	15	US-10-410-648-7
5	2373	99.5	455	9	US-09-771-956-30
6	2368	99.3	455	14	US-10-274-851-7
7	2330	97.7	445	14	US-10-027-049-6
8	2330	97.7	445	14	US-10-225-567A-205
9	2330	97.7	445	14	US-10-295-027-668
10	2330	97.7	445	15	US-10-181-906-14
11	2326	97.5	499	9	US-09-771-956-9
12	2321	97.3	445	10	US-09-826-509-533
13	2084.5	87.4	456	9	US-09-962-646-2
14	2074.5	87.0	445	14	US-10-027-049-4

15	2067.5	86.7	445	14	US-10-027-049-2	Sequence 2, Appli
16	2030.5	85.1	499	9	US-09-771-956-24	Sequence 24, Appl
17	2017	84.6	508	9	US-09-771-956-22	Sequence 22, Appl
18	1671	70.1	334	9	US-09-962-646-6	Sequence 6, Appli
19	1668.5	70.0	350	9	US-09-771-956-6	Sequence 6, Appli
20	1609.5	67.5	394	9	US-09-771-956-10	Sequence 10, Appl
21	1609.5	67.5	394	14	US-10-013-846-17	Sequence 17, Appl
22	1609.5	67.5	394	15	US-10-410-648-17	Sequence 17, Appl
23	1587.5	66.6	394	14	US-10-274-851-17	Sequence 17, Appl
24	1575.5	66.1	341	9	US-09-771-956-20	Sequence 20, Appl
25	1533.5	64.3	352	9	US-09-771-956-23	Sequence 23, Appl
26	1531.5	64.2	341	9	US-09-771-956-26	Sequence 26, Appl
27	1525.5	64.0	383	9	US-09-771-956-21	Sequence 21, Appl
28	1479.5	62.0	383	9	US-09-771-956-27	Sequence 27, Appl
29	1479.5	62.0	395	9	US-09-771-956-25	Sequence 25, Appl
30	497	20.8	371	14	US-10-081-810-49	Sequence 49, Appl
31	481.5	20.2	384	9	US-09-771-956-2	Sequence 2, Appli
32	481.5	20.2	384	10	US-09-393-896-23	Sequence 23, Appl
33	481.5	20.2	384	14	US-10-013-846-4	Sequence 4, Appli
34	481.5	20.2	384	14	US-10-176-847-26	Sequence 26, Appl
35	481.5	20.2	384	14	US-10-225-567A-378	Sequence 378, App
36	481.5	20.2	384	14	US-10-309-515-10	Sequence 10, Appl
37	481.5	20.2	384	14	US-10-177-293-330	Sequence 330, App
38	481.5	20.2	384	14	US-10-060-369-10	Sequence 10, Appl
39	481.5	20.2	384	14	US-10-291-390-31	Sequence 31, Appl
40	481.5	20.2	384	14	US-10-126-764-10	Sequence 10, Appl
41	481.5	20.2	384	14	US-10-295-027-640	Sequence 640, App
42	481.5	20.2	384	14	US-10-295-027-746	Sequence 746, App
43	481.5	20.2	384	15	US-10-410-648-4	Sequence 4, Appli
44	481.5	20.2	388	15	US-10-181-906-6	Sequence 6, Appli
45	481	20.2	383	14	US-10-081-810-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-771-956-13
; Sequence 13, Application US/09771956
; Patent No. US200010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-956-13

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RESULT 2

US-09-962-646-4
; Sequence 4, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION:
; APPLICANT: GERALD, CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L.
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHEK, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR
; FILE REFERENCE: 1795/461668ZA
; CURRENT APPLICATION NUMBER: US/09/962,646
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/200,673
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566,096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349,025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-962-646-4

Query Match 100.0%; Score 2385; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 1e-191;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 7, Application US/10013846
; Publication No. US20030036652A1
; GENERAL INFORMATION:
; APPLICANT: Bakhavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Marlys
; TITLE OF INVENTION: Spiro[sobenzofuran-1,4'-piperidin]-3-ones and
; TITLE OF INVENTION: 3H-spiro[sobenzofuran-1,4'-piperidines
; FILE REFERENCE: N00.2001
; CURRENT APPLICATION NUMBER: US/10/013,846
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 455
; TYPE: PRT
; ORGANISM: homosapiens
US-10-013-846-7

Query Match 100.0%; Score 2385; DB 14; Length 455;
Best Local Similarity 100.0%; Pred. No. 1e-191;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFYSKQDYNMDELDDEYNNKTLATENNNTAATRNSDFPVWDYKSSVDDLOQYFLIGLYTF 60
Db 1 MSFYSKQDYNMDELDDEYNNKTLATENNNTAATRNSDFPVWDYKSSVDDLOQYFLIGLYTF 60
QY 61 VSLGFMGNLLIIMALKRKNOKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120
Db 61 VSLGFMGNLLIIMALKRKNOKTTVNFIGNLAFSDILVLFCSPPFTLTSVLLDQWFG 120
QY 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISSNLTANHGYFLIATVTLGFAI 180
Db 121 KVMCHIMPLOCVSVLSTLILISIAIVRYHMKHPISSNLTANHGYFLIATVTLGFAI 180
QY 181 CSPLPVFHSLVLEQTFGSALLSSRYLCVSWPDSYRIAFITISLLVQYILPLVCLTVS 240
Db 181 CSPLPVFHSLVLEQTFGSALLSSRYLCVSWPDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVCRSISCGLSNKENRLEENEMINLTLPKSKGQVLSGSHKWSYFICKHRRYS 300
Db 241 HTSVCRSISCGLSNKENRLEENEMINLTLPKSKGQVLSGSHKWSYFICKHRRYS 300
QY 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSDVHEL 360
Db 301 KKTACVLPAPERPSQENHSRIILPENFGSVRSQSSSKFIPGVPCTCFEIKPEENSDVHEL 360
QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420

QY 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455
Db 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455

RESULT 4

US-10-410-648-7
; Sequence 7, Application US/10410648
; Publication No. US20040072847A1
; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A.
; APPLICANT: Briemann, Harry L.
; APPLICANT: Darrow, James W.
; APPLICANT: De Lombaert, Stephanie W.
; APPLICANT: Hutchinson, Alan W.
; APPLICANT: Tran, Jennifer W.
; APPLICANT: Zheng, Xiaozhang W.
; APPLICANT: Elliott, Richard L.
; APPLICANT: Hammond, Marlys L.
; TITLE OF INVENTION: 3H-PIPERIDIN-1,4'-PIPERIDIN-3-ONES AND
; FILE REFERENCE: U 014539-7
; CURRENT APPLICATION NUMBER: US/10/410,648
; PRIOR FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-12-11
; PRIOR FILING DATE: 2001-12-11
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 455
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-410-648-7

Query Match 100.0%; Score 2385; DB 15; Length 455;
Best Local Similarity 100.0%; Pred. No. 1e-191;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOYLIGLYTF 60
Db 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOYLIGLYTF 60
QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120
QY 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
Db 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
QY 181 CSPLPVHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db 181 CSPLPVHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Db 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360
QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420
QY 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455
Db 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455

RESULT 5

US-09-771-956-30
; Sequence 30, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 30
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Cercopithecus aethiops
US-09-771-956-30

Query Match 99.5%; Score 2373; DB 9; Length 455;
Best Local Similarity 99.3%; Pred. No. 1e-190;
Matches 452; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOYLIGLYTF 60
Db 1 MSFYSKQDYNMDELDYVYKTLATENTATRNSDFFVWDYKSSVDDLOYLIGLYTF 60
QY 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120
Db 61 VSLGFMGNLLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLDQWFG 120
QY 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
Db 121 KVMCHIMPLOQVSVLVSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVTLGFAI 180
QY 181 CSPLPVHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
Db 181 CSPLPVHSLVELQETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVS 240
QY 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300
Db 241 HTSVCRSISCGLSNKENLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKHHRRYS 300
QY 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360
Db 301 KKTACVLPAPERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCTPEIKPEENS DVHEL 360
QY 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420
Db 361 RVKRSVTRIKKRSRSVFYRLTILILVFAVSWMPHLHFHVWTFDNDNLISNRHFKLVYCIC 420
QY 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455
Db 421 HLLGMSCCLNPILYGLFNNIGIKADLVSLIHCLHM 455

RESULT 6

US-10-274-951-7
; Sequence 7, Application US/10274851
; Publication No. US20030144290A1
; GENERAL INFORMATION:
; APPLICANT: Blum, Charles
; APPLICANT: Briemann, Harry
; APPLICANT: De Lombaert, Stephanie
; APPLICANT: Zheng, Xiaozhang
; TITLE OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE
; FILE REFERENCE: U 014209-8
; CURRENT APPLICATION NUMBER: US/10/274,851
; CURRENT FILING DATE: 2002-10-21

NUMBER OF SEQ ID NOS: 17
 SOFTWARE: Patent in Ver. 2.0
 SEQ ID NO 7
 LENGTH: 455
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-274-851-7

Query Match 99.3%; Score 2368; DB 14; Length 455;
 Best Local Similarity 99.6%; Pred. No. 2.7e-190;
 Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MFYSKQDYNMDELDYNNKTLATNTAATRNDDFPVDDYKSSVDDQYFLGLYTF 60
Db 1 MFYSKQDYNMDELDYNNKTLATNTAATRNDDFPVDDYKSSVDDQYFLGLYTF 60
QY 61 VSLGFMGNLLILMALMKRNQKTTNVLGNLAFSDILVLFCSPTLTSLVLDQWFG 120
Db 61 VSLGFMGNLLILMALMKRNQKTTNVLGNLAFSDILVLFCSPTLTSLVLDQWFG 120
QY 121 KVMCHMPFLQCVSLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGF 180
Db 121 KVMCHMPFLQCVSLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGF 180
QY 181 CSPLPVHSLVQLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
Db 181 CSPLPVHSLVQLQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVS 240
QY 241 HTSVCRSISGSLNKENLEENEMINLTLPKSKGPGQVLSGSHKWSYSFIKRRRYS 300
Db 241 HTSVCRSISGSLNKENLEENEMINLTLPKSKGPGQVLSGSHKWSYSFIKRRRYS 300
QY 301 KKTACVLPAPEPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360
Db 301 KKTACVLPAPEPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHEL 360
QY 361 RYKRSVTRIKRSRVFYRLTILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
Db 361 RYKRSVTRIKRSRVFYRLTILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCIC 420
QY 421 HLLGMMSCCLNPILYGFNLNGIKADLVSLIHLHM 455
Db 421 HLLGMMSCCLNPILYGFNLNGIKADLVSLIHLHM 455

```

RESULT 7

US-10-027-049-6
 Sequence 6, Application US/10027049
 Publication No. US2003002283A1
 GENERAL INFORMATION:
 APPLICANT: Hu Ph.D., Yinghe
 McCaleb Ph.D., Michael L.
 Bloomquist Ph.D., Brian T.
 Flores-Riveros Ph.D., Jaime R.
 Cornfield Ph.D., Linda J.
 TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid Sequences
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boenken Hulbert & Berghoff
 STREET: 300 South Wacker Drive, 32nd Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/027,049
 FILING DATE: 08-Apr-1996

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Greenfield Ph.D., Michael S.
 REGISTRATION NUMBER: 37,142
 REFERENCE/DOCKET NUMBER: 96,149/WH 405
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 715-1000
 TELEFAX: (312) 715-1234

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 445 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-027-049-6

Query Match 97.7%; Score 2330; DB 14; Length 445;
 Best Local Similarity 100.0%; Pred. No. 4.1e-187;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 11 MDLEDEYNNKTLATNTAATRNDDFPVDDYKSSVDDQYFLGLYTFVSLGFMGNL 70
Db 1 MDLEDEYNNKTLATNTAATRNDDFPVDDYKSSVDDQYFLGLYTFVSLGFMGNL 60
QY 71 LILMALMKRNQKTTNVLGNLAFSDILVLFCSPTLTSLVLDQWFGKVMCHMPFL 130
Db 61 LILMALMKRNQKTTNVLGNLAFSDILVLFCSPTLTSLVLDQWFGKVMCHMPFL 120
QY 131 QCVSLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGFACSLPVFHS 190
Db 121 QCVSLVSTLILISIAIVRYHMKHPIISNNLTANHGYFLIATVMTLGFACSLPVFHS 180
QY 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRS 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRS 240
QY 251 GLSNKENRLEENEMINLTLPKSKGPGQVLSGSHKWSYSFIKRRRYSKKTACVLPA 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPGQVLSGSHKWSYSFIKRRRYSKKTACVLPA 300
QY 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
Db 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360
QY 371 KRSRVYFRLTILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGMMSCCL 430
Db 361 KRSRVYFRLTILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYCICHLGMMSCCL 420
QY 431 NFILYGFNLNGIKADLVSLIHLHM 455
Db 421 NFILYGFNLNGIKADLVSLIHLHM 445

```

RESULT 8

US-10-225-567A-205
 Sequence 205, Application US/10225567A
 Publication No. US20030113798A1
 GENERAL INFORMATION:
 APPLICANT: LifeSpan Biosciences
 APPLICANT: Brown, Joseph P.
 APPLICANT: Burner, Glenna C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 205
 LENGTH: 445

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-205

Query Match
Best Local Similarity 97.7%; Score 2330; DB 14; Length 445;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MDLEDEYVYKTLATENNNTAATNSDFFPWDDYKSSVDDLOQYFLGLTYFVSLGFMGNL 70
Db 1 MDLEDEYVYKTLATENNNTAATNSDFFPWDDYKSSVDDLOQYFLGLTYFVSLGFMGNL 60

Qy 71 LILMALMKKNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 130
Db 61 LILMALMKKNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 120

Qy 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGCFYLIATWTWLGFAICSPPLVHFSL 190
Db 121 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGCFYLIATWTWLGFAICSPPLVHFSL 180

Qy 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 240

Qy 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFVKHRRYSKKTACVLPAP 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFVKHRRYSKKTACVLPAP 300

Qy 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
Db 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360

Qy 371 KRRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 430
Db 361 KRRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 420

Qy 431 NPILYGLFNGIKADLVSLIHCLHM 455
Db 421 NPILYGLFNGIKADLVSLIHCLHM 445

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RESULT 9

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US-10-295-027-668
; Sequence 668, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14

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; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 668
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-668

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Query Match 97.7%; Score 2330; DB 14; Length 445;
Best Local Similarity 100.0%; Pred. No. 4.1e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MDLEDEYVYKTLATENNNTAATNSDFFPWDDYKSSVDDLOQYFLGLTYFVSLGFMGNL 70
Db 1 MDLEDEYVYKTLATENNNTAATNSDFFPWDDYKSSVDDLOQYFLGLTYFVSLGFMGNL 60

Qy 71 LILMALMKKNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 130
Db 61 LILMALMKKNQKTTVNFIGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 120

Qy 131 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGCFYLIATWTWLGFAICSPPLVHFSL 190
Db 121 QCVSVLVSTLILISIAIVRYHMKHPISNNLTANHGCFYLIATWTWLGFAICSPPLVHFSL 180

Qy 191 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 250
Db 181 VELQETFGSALLSSRYLCVESWPSDSYRIAFITISLLVQYILPLVCLTVSHTSVCRSISC 240

Qy 251 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFVKHRRYSKKTACVLPAP 310
Db 241 GLSNKENRLEENEMINLTLPKSKGPOVKLSGSHKWSYFVKHRRYSKKTACVLPAP 300

Qy 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 370
Db 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKSVTRIK 360

Qy 371 KRRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 430
Db 361 KRRSRVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMSCL 420

Qy 431 NPILYGLFNGIKADLVSLIHCLHM 455
Db 421 NPILYGLFNGIKADLVSLIHCLHM 445

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RESULT 10

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US-10-181-906-14
; Sequence 14, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
; APPLICANT: Karsenty, Gerard
; APPLICANT: Amling, Michael
; APPLICANT: Ducey, Patricia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
; TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY
; FILE REFERENCE: 9142-020-999
; CURRENT APPLICATION NUMBER: US/10/181,906
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/02040
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 445

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-181-906-14

Query Match      97.7%; Score 2330; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 4.1e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTFVSLIGFMGNL 70
DB 1 MDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTFVSLIGFMGNL 60

QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMGMCHMPPFL 130
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMGMCHMPPFL 120

QY 131 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYPFLIATVMTLGFALCSPLPVHSL 190
DB 121 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYPFLIATVMTLGFALCSPLPVHSL 180

QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250
DB 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240

QY 251 GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPA 310
DB 241 GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPA 300

QY 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSLVRSVTRIK 370
DB 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSLVRSVTRIK 360

QY 371 KRSRSVFRLLTILILVFAVSWMPLHLFHVVDTFDNDNLISNRHFKLVYICHLIGMSSCL 430.
DB 361 KRSRSVFRLLTILILVFAVSWMPLHLFHVVDTFDNDNLISNRHFKLVYICHLIGMSSCL 420

QY 431 NPILYGFLNNGIKADLVSLIHCLHM 455
DB 421 NPILYGFLNNGIKADLVSLIHCLHM 445

RESULT 11
US-09-771-956-9
; Sequence 9, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodebeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA
US-09-771-956-9

Query Match      97.5%; Score 2326; DB 9; Length 499;
Best Local Similarity 99.6%; Pred. No. 1e-186;
Matches 444; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFYSKQDYNMDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTF 60
DB 1 MSFYSKQDYNMDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTF 60

QY 61 VSLIGFMGNLILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMG 120

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-181-906-14

Query Match      97.7%; Score 2330; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 4.1e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTFVSLIGFMGNL 70
DB 1 MDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTFVSLIGFMGNL 60

QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMGMCHMPPFL 130
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMGMCHMPPFL 120

QY 131 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYPFLIATVMTLGFALCSPLPVHSL 190
DB 121 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYPFLIATVMTLGFALCSPLPVHSL 180

QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250
DB 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240

QY 251 GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPA 310
DB 241 GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPA 300

QY 311 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSLVRSVTRIK 370
DB 301 ERPSQENHSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHSLVRSVTRIK 360

QY 371 KRSRSVFRLLTILILVFAVSWMPLHLFHVVDTFDNDNLISNRHFKLVYICHLIGMSSCL 430.
DB 361 KRSRSVFRLLTILILVFAVSWMPLHLFHVVDTFDNDNLISNRHFKLVYICHLIGMSSCL 420

QY 431 NPILYGFLNNGIKADLVSLIHCLHM 455
DB 421 NPILYGFLNNGIKADLVSLIHCLHM 445

RESULT 12
US-09-826-509-533
; Sequence 533, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 533
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-533

Query Match      97.3%; Score 2321; DB 10; Length 445;
Best Local Similarity 99.8%; Pred. No. 2.3e-186;
Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTFVSLIGFMGNL 70
DB 1 MDLEDEYNTKLTATNTAATNSDPFVWDYKSSVDDLOQYFLIGLYTFVSLIGFMGNL 60

QY 71 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMGMCHMPPFL 130
DB 61 LILMALMKRNQKTTVNFIGNLAFSDILVLFCSPPFTLTSLVLDQWFMGMCHMPPFL 120

QY 131 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYPFLIATVMTLGFALCSPLPVHSL 190
DB 121 QCVSVLVSTLILISIAIVRYHMKHPIISNNLTANHGYPFLIATVMTLGFALCSPLPVHSL 180

QY 191 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 250
DB 181 VELOETFGSALLSSRYLCVESWPSDSYRIAFTISLLVQYILPLVCLTVSHTSVCRSISC 240

QY 251 GLSNKENRLEENEMINTLHPSKSGPOVKLSGSHKWSYFIKKHRRYSKKTACVLPA 310

```

Db 241 GLSKENRLEENEMINLTLPKSKSQPVKLSGSHKWSYSFTKKHRRYSKKTACVLFPAP 300
Qy 311 ERPSQNHRSRILPENFGSVRSQSSSKFIPGVPTCFIKKPEKNSDVHKLAVKSVTRIK 370
Db 301 ERPSQNHRSRILPENFGSVRSQSSSKFIPGVPTCFIKKPEKNSDVHKLAVKSVTRIK 360
Qy 371 KRGRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGWSGCL 430
Db 361 KRGRSVFYRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGWSGCL 420
Qy 431 NPILYGLFNGIKADIVSLIHCLHM 455
Db 421 NPILYGLFNGIKADIVSLIHCLHM 445

RESULT 13
US-09-962-646-2
; Sequence 2, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION:
; APPLICANT: GERALD, CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L.
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHER, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
; FILE REFERENCE: 1795/46166BZA
; CURRENT APPLICATION NUMBER: US/09/962,646
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/200,673
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566,096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349,025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 456
; ORGANISM: Rattus No. US20020103123A1vegicus
US-09-962-646-2

Query Match 87.4%; Score 2084.5; DB 9; Length 456;
Best Local Similarity 88.2%; Pred. No. 1.8e-166;
Matches 396; Conservative 22; Mismatches 30; Indels 1; Gaps 1;

Qy 7 QDYNMDELDEYNNKTLATENNNTAATRNSDPVDYKSSVDDLYQYFLIGLYTFVSLIGF 66
Db 8 QDSSMEFKLEEHNKTFVTENNTAARNAAPAWEDYRGSVDDLYQYFLIGLYTFVSLIGF 67

Qy 67 MGNLLILMALMKRQKTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHI 126
Db 68 MGNLLILMALMKRQKTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHI 127

Qy 127 MPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFACSPLPV 186
Db 128 MPFLQCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFACSPLPV 187

Qy 187 FHSVLQTFGSALLSSRYLCVSWPDSYRIAPTISLLVQVILPLVCLTVSHTSVCR 246
Db 188 FHSVLQTFGSALLSSRYLCVSWPDSYRIAPTISLLVQVILPLVCLTVSHTSVCR 247

Qy 247 SISCGLSNKENLEENEMINLTLPKSKSQPVKLSGSHKWSYSFTKKHRRYSKKTACV 306
Db 248 SISCGLSNKENLEENEMINLTLPKSKSQPVKLSGSHKWSYSFTKKHRRYSKKTACV 307

Qy 307 LPAPERPSQENSRILPENFGSVRSQSSSKFIPGVPTCFIKKPEKNSDVHKLAVKSV 366
Db 308 LPAPERPSQENSRILPENFGSVRSQSSSKFIPGVPTCFIKKPEKNSDVHKLAVKSV 366

Qy 367 TRIKRSRSVFRILTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGWM 426

Db 367 TRIKRSRSVFRILTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICHLGWM 426
Qy 427 SCCLPILYGLFNGIKADIVSLIHCLHM 455
Db 427 SCCLPILYGLFNGIKADIVSLIHCLHM 455

RESULT 14
US-10-027-049-4
; Sequence 4, Application US/10027049
; Publication No. US2003002283A1
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; McCaleb Ph.D., Michael L.
; Bloomquist Ph.D., Brian T.
; Flores-Riveros Ph.D., Jaime R.
; Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/027,049
; FILING DATE: 08-Apr-1996
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Greentield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1000
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-027-049-4

Query Match 87.0%; Score 2074.5; DB 14; Length 445;
Best Local Similarity 88.5%; Pred. No. 1.2e-165;
Matches 394; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

Qy 11 MDELDEYNNKTLATENNNTAATRNSDPVDYKSSVDDLYQYFLIGLYTFVSLIGF 70
Db 1 MEFKLEENKTFVTENNTAARNAAPAWEDYRGSVDDLYQYFLIGLYTFVSLIGF 60

Qy 71 LILMALMKRQKTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHI 130
Db 61 LILMALMKRQKTTWNFLGNLAFSDILVLFCSPTLTSVLLDQWFGKVMCHI 120

Qy 131 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFACSPLPV 190
Db 121 QCVSVLSTLILISIAIVRYHMKHPISNNLTANHGYFLIATVMTLGFACSPLPV 180

Qy 191 VELQTFGSALLSSRYLCVSWPDSYRIAPTISLLVQVILPLVCLTVSHTSVCR 250
Db 181 VELQTFGSALLSSRYLCVSWPDSYRIAPTISLLVQVILPLVCLTVSHTSVCR 240

QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIRKRRRYSKKTACVLPAP 310
 Db 241 GLSHKENRLEENEMINLTLPKSKSRNOAKTPSTQKWSYFIRKRRRYSKKTACVLPAP 300
 QY 311 ERPSQENHRSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKRSVTRIK 370
 Db 301 AGPSQOKHLAV-PENPASVRSQSSSKVPGVPICFEVKPESSDAHEMRVRSITRIK 359
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 430
 Db 360 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 419
 QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455
 Db 420 NPILYGLFNNGIKADLVSLIHCLHM 444

RESULT 15

US-10-027-049-2

; Sequence 2, Application US/10027049

; Publication No. US2003002283A1

; GENERAL INFORMATION:

; APPLICANT: Hu Ph.D., Yinghe

; McCaleb Ph.D., Michael L.

; Bloomquist Ph.D., Brian T.

; Flores-Riveros Ph.D., Jaime R.

; Cornfield Ph.D., Linda J.

; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

; Sequences

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive, 32nd Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/027,049

; FILING DATE: 08-Apr-1996

; CLASSIFICATION: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Greenfield Ph.D., Michael S.

; REGISTRATION NUMBER: 37,142

; REFERENCE/DOCKET NUMBER: 96,149/WH 405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312)715-1000

; TELEFAX: (312)715-1234

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-027-049-2

Query Match

Best Local Similarity 86.7%; Score 2067.5; DB 14; Length 445;

Matches 393; Conservative 21; Mismatches 30; Indels 1; Gaps 1;

QY 11 MDLELDYNNKTLATENTNATRNSDPFVWDDYKSSVDDIQYELIGLYTFVSLGFMGNL 70
 Db 1 MEFKLEHFNKTFVTENTNATRNAPFAWEDYRGSDVDDQYELIGLYTFVSLGFMGNL 60
 QY 71 LILMALMKKNQKNTVNFNLGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 130
 Db 61 PILMAVMKKNQKNTVNFNLGNLAFSDILVLFCSPTLTSLVLLDQWFGKVMCHIMPFL 120

QY 131 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYELIATVWTLGFAICSPVPVHSL 190
 Db 121 QCVSVLVSTLILISIAIVRYHMIKHPISNNLTANHGYELIATVWTLGFAICSPVPVHSL 180
 QY 191 VELQETFGSALLSRVLCVESWPSDSYRIAFITISLLLVQVILPLVCLTVSHTSVCRSISC 250
 Db 181 VELKETFGSALLSKYLCVESWPSDSYRIAFITISLLLVQVILPLVCLTVSHTSVCRSISC 240
 QY 251 GLSNKENRLEENEMINLTLPKSKSGPOVKLSGSHKWSYFIRKRRRYSKKTACVLPAP 310
 Db 241 GLSHKENRLEENEMINLTLPKSKSRNOAKTPSTQKWSYFIRKRRRYSKKTACVLPAP 300
 QY 311 ERPSQENHRSRILPENFGSVRSQSSSKFIPGVPTCFEIKPEENSDVHELVRKRSVTRIK 370
 Db 301 AGPSQOKHLAV-PENPASVRSQSSSKVPGVPICFEVKPESSDAHEMRVRSITRIK 359
 QY 371 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 430
 Db 360 KRSRSVYFRLTILILVFAVSWMPLHLFHVVTDFNDNLISNRHFKLVYICICHLGMMSCCL 419
 QY 431 NPILYGLFNNGIKADLVSLIHCLHM 455
 Db 420 NPILYGLFNNGIKADLVSLIHCLHM 444

Search completed: October 21, 2004, 12:17:03
 Job time : 130 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 21, 2004, 11:29:39 ; Search time 205 Seconds

(without alignments)
4920.716 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480

Sequence: 1 ttttggttgctgacaaatgt.....attctcaactgtttaccaagg 1406

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=A_Geneseq_23Sep04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MWAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	96.2	455	2 AAR95939	Aar95939 Human Y5
2	2385	96.2	455	2 AAW29447	Aaw29447 Human hip
3	2385	96.2	455	2 AAW29413	Aaw29413 Human hip
4	2385	96.2	455	2 AAW37093	Aaw37093 Homo sapi
5	2385	96.2	455	2 AAY57461	Aay57461 Human hip
6	2385	96.2	455	4 AAE08002	Aae08002 Human neu
7	2385	96.2	455	5 ABB84497	Abb84497 Human hip
8	2385	96.2	455	5 ABB79510	Abb79510 Human neu
9	2385	96.2	455	5 ABO23266	Abo23266 Human neu
10	2385	96.2	455	8 ADO29564	Ado29564 Human GPC

11	2373	95.7	455	4 AAE08016	Aae08016 African g
12	2330	94.0	445	2 AAW27604	Aaw27604 Human neu
13	2330	94.0	445	2 AAW15230	Aaw15230 Human neu
14	2330	94.0	445	2 AAY14554	Aay14554 Human neu
15	2330	94.0	445	3 AAY52578	Aay52578 Human NPY
16	2330	94.0	445	4 AAE07958	Aae07958 Human neu
17	2330	94.0	445	4 AAE06692	Aae06692 Human neu
18	2330	94.0	445	4 AAE07922	Aae07922 Human neu
19	2330	94.0	445	4 AAB85121	Aab85121 Human neu
20	2330	94.0	445	4 AAB85110	Aab85110 Human neu
21	2330	94.0	445	6 ABB81860	Abb81860 Human neu
22	2330	94.0	445	7 ADN39350	Adn39350 Cancer/chi
23	2326	93.8	499	4 AAE08004	Aae08004 Human chi
24	2326	93.8	499	5 ABB32254	Abb32254 Neuropst
25	2321	93.6	445	4 ABB56370	Abb56370 Non-endog
26	2318	93.5	445	4 AAE02851	Aae02851 Rhesus ne
27	2266	91.4	445	3 AAY52577	Aay52577 Chimeric
28	2262	91.2	456	2 AAW37095	Aaw37095 Canis dom
29	2084.5	84.1	456	2 AAR95940	Aar95940 Rat Y5 re
30	2084.5	84.1	456	2 AAW29446	Aaw29446 Rat hypot
31	2084.5	84.1	456	2 AAW29412	Aaw29412 Rat hypot
32	2084.5	84.1	456	2 AAW37092	Aaw37092 Rattus no
33	2084.5	84.1	456	2 AAY57460	Aay57460 Rat hypot
34	2084.5	84.1	456	5 ABB84496	Abb84496 Rat hypot
35	2074.5	83.6	445	2 AAW27603	Aaw27603 Rat neuro
36	2074.5	83.6	445	2 AAY14553	Aay14553 Rat neuro
37	2074.5	83.6	445	3 AAY52579	Aay52579 Rat NPY (
38	2074	83.6	466	2 AAW15233	Aaw15233 Mouse neu
39	2072.5	83.6	445	2 AAW15232	Aaw15232 Rat neuro
40	2070	83.5	466	8 ADO29565	Ado29565 Mouse GPC
41	2067.5	83.4	445	2 AAW27602	Aaw27602 Rat neuro
42	2067.5	83.4	445	2 AAY14552	Aay14552 Rat neuro
43	2030.5	81.9	499	4 AAE08012	Aae08012 Rat chine
44	2017	81.3	508	4 AAE08010	Aae08010 Mouse chi
45	1671	67.4	334	2 AAR95941	Aar95941 Canine Y5

ALIGNMENTS

RESULT 1
AAR95939
ID AAR95939 standard; protein; 455 AA.

XX	AC	AAR95939;		
XX	DT	14-OCT-1996 (first entry)		
XX	DE	Human Y5 receptor.		
XX	KW	Y5 receptor; atypical neuropeptide Y1 receptor; feeding behavior;		
KW	KW	G protein-coupled receptor; agonist; antagonist; obesity; bulimia;		
KW	KW	anorexia; transgenic animal.		
XX	OS	Homo sapiens.		
XX	PH	Key	Location/Qualifiers	
FT	FT	Domain	51..77	
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FT	FT		/note= "transmembrane domain I"	
FT	FT	Domain	88..110	
FT	FT		/label= II	
FT	FT	Domain	126..147	
FT	FT		/note= "transmembrane domain II"	
FT	FT		/label= III	
FT	FT		/note= "transmembrane domain III"	
FT	FT	Domain	166..187	
FT	FT		/label= IV	
FT	FT		/note= "transmembrane domain IV"	
FT	FT	Domain	220..242	
FT	FT		/label= V	
FT	FT		/note= "transmembrane domain V"	
FT	FT	Domain	380..403	
FT	FT		/label= VI	

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FT      /note= "transmembrane domain VI"
FT      416..438
FT      /label= VII
FT      /note= "transmembrane domain VII"
XX      WO9616542-A1.
XX      06-JUN-1996.
XX      01-DEC-1995; 95WO-US015646.
XX      02-DEC-1994; 94US-00349025.
XX      (SYNA-) SYNAPTIC PHARM CORP.
XX      Gerald CPG, Walker MW, Branchek T, Weinshank RL;
XX      WPI: 1996-277371/28.
XX      N-PSDB; AAT30433.
XX      Modifying feeding behaviour using Y5 receptor (ant)agonists - increases
XX      or decreases food consumption, for treatment of e.g. obesity or bulimia.
XX      Claim 51; Fig 6; 235pp; English.
XX      Human hippocampal Y5 receptor (AAR95939) was identified as the homologue
XX      of rat hypothalamic Y5 receptor (AAR95940), isolated as an 'atypical Y1
XX      receptor'. The receptor belongs to the G protein-coupled receptor
XX      superfamily. It is encoded by a cDNA clone (see also AAT30433) that was
XX      isolated from a hippocampus cDNA library using rat Y5 receptor cDNA as
XX      probe. Recombinant rat Y5 receptor can be produced in prokaryotic or
XX      eukaryotic (e.g. COS, 293 or Sf9 insect) host cells. It is used to
XX      identify Y5 ligands (agonists and antagonists) that can be used to treat
XX      obesity, bulimia or anorexia, and to raise monoclonal antibodies useful
XX      in detecting Y5 receptor
XX      SQ      Sequence 455 AA;

Alignment Scores:
Pred. No.:      1.34e-253      Length:      455
Score:          2385.00      Matches:      455
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      96.17%      Indels:      0
DB:              2      Gaps:      0

US-09-771-956-4 (1-1406) x AAR95939 (1-455)
QY      17 ATGCTCTTTTATTCACAGCAGGACTAATAATGATTAGAGCTCGACGAGTATTATAAC 76
DB      1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
QY      77 AAGACACTGCCACAGAGATAATACTGTCGCCACTCGGAATTCGATTTCCAGCTCTGG 136
DB      21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
QY      137 GATGACTATAAAGCAGCTGTAGTAGCTTACAGTATTCTTGATTTGGCTCTATACATTT 196
DB      41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuLeuGlyLeuTyrThrPhe 60
QY      197 GTAAGCTCTCTGCTTTATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAAGCGT 256
DB      61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
QY      257 AATCAGAAAGACTACGGTAACCTTCATAGGCAATCTGGCCTTTCTGATATCTTGGTT 316
DB      81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY      317 GTGCTGTTTGTCTACCTTTTACACTGACGCTCTGCTTGTGTCGATCAGTGGATGTTTGGC 376
DB      101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY      377 AAAGTCATGTGCCATATATGCGCTTTTCTTCAATATGTGTGTCAGTTTGGTTTCACTTTA 436
DB      121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY      437 ATTTTAATATCAATGCCATTTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT 496
DB      141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
QY      497 TTAACAGCAAAACCATGGCTACTTTCTGATAGTACTGCTCGACACTAGGTTTCCCATC 556
DB      161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
QY      557 TGTTCCTCCCTTCCAGTGTTCACAGTCTTGTGGAACITTCAGAAACATTTGGTTCAGCA 616
DB      181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
QY      617 TTGCTGACGACGACGAGTATTATTTAGTTGAGTCATGGCCATCTGATTCATACAGATTGCC 676
DB      201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY      677 TTTACTATCTCTTTTATTTGCTAGTTTCTGAGTATATTTGCGCTTATGTTGTTTACTTAAGT 736
DB      221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
QY      737 CATACAAAGTGTCTGCAGAAAGTATAAGCTGTGGATTGTCCAAAGAAACACAGACTTGA 796
DB      241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
QY      797 GAAATGAGATCATCAACTTAACCTTTCATCCATCCAAAGAGTGGCGCTCAGGTGAAA 856
DB      261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
QY      857 CTCTCTGGCAGCCATAAATGGAGTTATTTCATTCATCAAAAAACACAGAAAGATATAGC 916
DB      281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
QY      917 AAGAAGACAGCATGTGTGTACCTGCTCCAGAAAGACCTTCTCAGAGAAACCACTCCAGA 976
DB      301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
QY      977 ATACTTCCAGAAAACTTTGGCTCTCTAAGAAAGTCTCAGCTCTCTTCATCCAGTAAGTTTCA 1036
DB      321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
QY      1037 CCAGGGTCCCGACTTGTCTTTCAGATATAAACTGAGAAATTCAGATGTTTCATGAATTG 1096
DB      341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360
QY      1097 AGAGTAAAAACGTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTTCCTCAGACTG 1156
DB      361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
QY      1157 ACCACTAGTATATTAGTATTGCTGTAGTTGGATGGCACTACACCTTTCCATGTGGTA 1216
DB      381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY      1217 ACTGATTTTAATGCAATCTTATTTCAAATAGGCAATTCAGTTGGTGTGTTGCTATTTGT 1276
DB      401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY      1277 CATTTGTTGGCATGATGCTCTGTGTCTTAAATCCAAATCTTATATGGGTTTCTTAATAAT 1336
DB      421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY      1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381
DB      441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 2
AAW29447
ID      AAW29447
XX      standard; protein; 455 AA.
XX      AC      AAW29447;
XX      XX

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DT	25-MAR-2003 (revised)		61	ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuLeuMetAlaLeuMetLysArg	80
DT	26-FEB-1998 (first entry)		257	ANTCAGAACTACGGTAAACTTCTCATAGCAATCTGGCTTTCTGATATCTGGTT	316
XX	Human hippocampal neuropeptide Y Y5 receptor.		81	AsnGlnLysThrValAsnPheLeuLeuGlyAsnLeuAlaPheSerAspLeuVal	100
XX	Hippocampal; neuropeptide Y Y5 receptor; NPY Y5; antagonist;		317	GTGCTGTTTGTCTCACCTTTACACTGACGTCTGCTGCGATCAGTGAATGTTGGC	376
XX	epileptic seizure; migraine; sleep disturbance; prophylaxis;		101	ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly	120
XX	eating disorder; quinoxalin-2,4-diazirine.		377	AAAGTCATGCGCATATATGCTTTCTCAATGTGTGTCAGTTTGGTTTCAACTTGA	436
OS	Homo sapiens.		121	LysValMetCysHisLeuMetProPheLeuGlnCysValSerValLeuValSerThrLeu	140
XX	WO9720822-A1.		437	ATTTTAATATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAT	496
XX	12-JUN-1997.		141	IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn	160
XX	18-NOV-1996; 96WO-EP005066.		497	TTAACAGCAACCATGGCTACTTCTGTAGTACTGCTGCACACTAGGTTTGGCCATC	556
XX	01-DEC-1995; 95US-00566027.		161	LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle	180
XX	(NOVS) NOVARTIS AG.		557	TGTTCTCCCTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTGAGA	616
XX	Rueger H. Schmidlin T. Rigollier P. Yamaguchi Y;		181	CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla	200
XX	Tintinotblomley M, Schilling W, Criscione L;		617	TTGCTCAGCAGCAGGATTTTGTGTAGTGTATGCGCATCTGATTCATACAGATTTGCC	676
XX	WP1; 1997-319712/29.		201	LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla	220
XX	N-PSDB; AA89114.		677	TTTACTATCTCTTTATTGCTAGTTCAGTATATTCGCCCTTAGTTTGTCTTACTGTAAGT	736
XX	Use of new and known quinoxalin-2,4-diazirine compounds as NPY Y5		221	PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer	240
XX	receptor antagonists - for treating and preventing eating disorders,		737	CATACAAGTGTCTGCAGAAAGTATAAGCTGTGATTTGTCCAAAGAAAGAAACAGACTTGA	796
XX	diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,		241	HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu	260
XX	migraine, sleep disturbance, etc.		797	GAATAAGATGATCAACTTAATCTTCTCATCCATCCAAAGAGTGGGCTCAGGTGAAA	856
XX	Disclosure; Page 127-129; 155pp; English.		261	GluAsnGluMetIleAsnLeuThrLeuHisProSerLysSerGlyProGlnValLys	280
XX	The present sequence represents human hippocampal neuropeptide (NP) Y		857	CTCTCTGGAGCCATAAATGGAGTTATTTCATTCATCAAAAAACACAGAGAAGATATAGC	916
XX	receptor subtype Y5, with a pharmacological function associated with for		281	LeuSerGlySerHisLysTrpSerTyrSerPheIleLysHisArgArgTyrSer	300
XX	example, obesity and eating disorders. The specification relates to a		917	AAGAAGACAGCATGTGTGTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA	976
XX	method of treatment and prophylaxis of disorders and diseases associated		301	LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg	320
XX	with NPY receptor subtype Y5 comprising administering to a warm-		977	ATACTTCCAGAAACTTTGGCTCTGTAAGAAGTTCAGCTCTCTTTCATCCAGTAACTTATA	1036
XX	blooded animal, including man, in need of such treatment a		321	IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle	340
XX	therapeutically effective amount of a quinoxalin-2,4-diazirine compound.		1037	CCAGGGGTCCCACTTGTGTTGAGATAAAACCTGAAAGAAATTCAGATGTTTCATGATTC	1096
XX	These disorders and diseases include e.g. eating disorders, obesity,		341	ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu	360
XX	bulimia nervosa, diabetes, dyslipidaemia, hypertension, memory loss,		1097	AGAGTAAGAGCTTCTGTTACAGAAATAAAAGAGATCTCGAAGTGTCTTCTACAGACTG	1156
XX	epileptic seizures, migraine, sleep disturbance, pain,		361	ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu	380
XX	sexual/reproductive disorders, depression, anxiety, cerebral haemorrhage,		1157	ACCATCTGATATATGATTTGCTGTAGTGTGATGCCATCCACTACACCTTTTCCATGCGTA	1216
XX	CC shock, congestive heart failure, nasal congestion or diarrhoea. (Updated		381	ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal	400
XX	on 25-MAR-2003 to correct PI field.)		1217	ACTGATTTTAAATGACAACTTATTTCAATAGCAATTCAGTTGGTGTATTCATTTGT	1276
XX			401	ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys	420
XX			1277	CATTGTTGGCATGATGCTCTGTTGTTCTTAATCCCAATCTATATGGGTTTCTTAATAAT	1336
SQ	Sequence 455 AA;				

Alignment Scores:		
Pred. No.:	1.34e-253	Length: 455
Score:	2385.00	Matches: 455
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	96.17%	Indels: 0
DB:	2	Gaps: 0

US-09-771-956-4 (1-1406) x AAW29447 (1-455)		
QY	17 ATGTCCTTTTATTCCAAGCAGCACTATAATATGATTTAGAGCTCGACGATTTATAAC	76
Db	1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuLeuAspGluTyrTyrAsn	20
QY	77 AAGACATTTGCCACAGAGAAATTAATCTGCTGCCATCCGAATTCGATTTCCAGTCTGG	136
Db	21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr	40
QY	137 GATGACTATAAAGCAGTGTAGATGACTTACAGTATTTTCTGATTTGGGCTCTATACATTT	196
Db	41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe	60
QY	197 GTAAGTCTTCTGGCTTTATGCGGAATCTACTTATTTAAATGGCTCTCATGAAAAAGCGT	256

QY	1097	AGAGTAAAAACGTTCTGCTTACAGAAATAAAAAAGAGATCTCGAAGTGTGTTCTTACAGACTG	1156
Db	361	ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu	380
QY	1157	ACCATCTCATATTAGTATTTCCTGTTAGTGGATGCCACTACACCTTTTCCATGTGCTA	1216
Db	381	ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal	400
QY	1217	ACTGATTTTAAATGACAATCTTATTTCAAATAGGCATTTCAAATGTGCTGTTATTCGATTGTT	1276
Db	401	ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys	420
QY	1277	CATTGTTGGCGATGATGCCTGTGTCTTTAATCCAAATCTATATGCGTTTCTTAATAAT	1336

Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyGlyPheLeuAsnAsn 440
 QY 1337 GGGATTAAGCTGATTAGTGTCCCTTATACACTGCTTCATATG 1381
 Db 441 GlyIleYsAlaAspLeuValSerLeuIleHisCysLeuHisMet 455
 RESULT 3
 AAW29413
 ID AAW29413 standard; protein; 455 AA.
 AC AAW29413;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-FEB-1998 (first entry)
 XX
 DE Human hippocampal neuropeptide Y Y5 receptor.
 XX
 KW Human hippocampal neuropeptide Y Y5 receptor; NPY Y5; prophylaxis;
 KW bulimia nervosa; diabetes; dyslipidaemia; hypertension; memory loss;
 KW epileptic seizure; migraine; sleep disturbance; pain; depression;
 KW sexual disorder; anxiety; cerebral haemorrhage, shock; diarrhoea;
 KW congestive heart failure; eating disorder; obesity.
 XX
 OS Homo sapiens.
 XX
 PN WO9720820-A1.
 XX
 PD 12-JUN-1997.
 XX
 PF 18-NOV-1996; 96WO-EP0050555.
 XX
 PR 01-DEC-1995; 95US-00566349.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Rueseger H, Schmidlin T, Rigollier P, Yamaguchi Y;
 PI Tinfelnotblomley M, Schilling W, Criscione L;
 XX
 XX WPI; 1997-319711/29.
 DR N-PSDB; AAT89110.
 XX
 XX Use of new and known hetero:aryl compounds as NPY Y5-receptor antagonists
 PT - for treating and preventing eating disorders, diabetes, dyslipidaemia,
 PT hypertension, memory loss, epilepsy, migraine, etc.
 XX
 PS Disclosure; Page 76-78; 155pp; English.
 XX
 CC This sequence represents human hippocampal neuropeptide (NP) Y receptor
 CC subtype Y5, with a pharmacological function associated with for example,
 CC obesity and eating disorders. The specification relates to a method of
 CC treatment and prophylaxis of disorders and diseases associated with
 CC NPY receptor subtype Y5 comprising administering to a warm-blooded
 CC animal, including man, in need of such treatment a therapeutically
 CC effective amount of a new heteroaryl compound. These disorders and
 CC diseases include e.g. eating disorders, obesity, bulimia nervosa,
 CC diabetes, dyslipidaemia, hypertension, memory loss, epileptic seizures,
 CC migraine, sleep disturbance, pain, sexual/reproductive disorders,
 CC depression, anxiety, cerebral haemorrhage, shock, congestive heart
 CC failure, nasal congestion or diarrhoea. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 455 AA;
 Alignment Scores:
 Pred No.: 1-34e-253 Length: 455
 Score: 2385.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 2 Gaps: 0
 US-09-771-956-4 (1-1406) x AAW29413 (1-455)

QY 17 ATGCTCTTTTATCCAGCAGGACTATAATATGGATTATAGCTCGCAGGATTTATAAC 76
 Db 1 MetSerPheTySerLysGlnAspTyAsnMetAspLeuGluLeuAspGluTyTyAsn 20
 QY 77 AAGACACTTCCACAGAGATATATCTGTGTCACACTCGGAATTTCTGATTTCCAGTCTCG 136
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrAsnSerAspPheProValTrp 40
 QY 137 GATGACTATAAAAGCAGGTGTAGATGACTTACAGTATTTCTGATTCGGCTCTATACATT 196
 Db 41 AspAspTyLysSerSerValAspLeuGlnTyPheLeuIleGlyLeuTyThrPhe 60
 QY 197 GTAAGTCTTCTGGCTTTATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAAGCT 256
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
 QY 257 AATCAGAACTACAGTAACTTCCTCATAGGCAATCTGGCTTTTCTGATATCTGGTT 316
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
 QY 317 GTGCTGTTTGTCTACCTTTACACTGAGCTGTCTGCTGTCGATCAGTGGATGTTGCG 376
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
 QY 377 AAAGTCATGTGCCATATTATGCTTTTCTCAATGTGTGTCTAGTTTGGTTTCAACTTTA 436
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 QY 437 ACTTTAATATCAATGCCATTTCTCAGGTATCATATGATAAAACATCCCATCTATTAAT 496
 Db 141 IleLeuIleSerIleAlaIleValArgTyHisMetIleLysHisProIleSerAsnAsn 160
 QY 497 TTAACAGCAACCATGGCTACTTTCTGATAGTACTGTCTGCACACTAGTTTTCCTATC 556
 Db 161 LeuThrAlaAsnHisGlyTyThrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
 QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTGTGTGGAACCTTCAAGAAACATTTGGTTGACGA 616
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
 QY 617 TTGCTGAGCAGCAGGTATTATGTCTGAGTCTGCGCATCTGATTCATACAGAAATTCGC 676
 Db 201 LeuLeuSerSerArgTyLeuCysValGluSerTrpProSerAspSerTyArgIleAla 220
 QY 677 TTTACTATCTTTTATGCTAGTCTAGTATATCTGCCCTTAGTTGTCTTACTGTAAAGT 736
 Db 221 PheThrIleSerLeuLeuValGlnTyIleLeuProLeuValCysLeuThrValSer 240
 QY 737 CATACAAGTGTCTGAGAGATATAGCTGTGGATTGTCCAAAGAAAGAAACAGACTTGAA 796
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 QY 797 GAAATGAGATGATCAACTTAACCTTTCATCCATCCAAAAAGAGTGGGCCTCAGGTGAAA 856
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
 QY 857 CTCTCTGCGCAGCATTAATGGAGTTTATTCATTCATCAAAAAACAGAGAGATATAGC 916
 Db 281 LeuSerGlySerHisLysTySerTySerPheIleLysLysHisArgArgTySer 300
 QY 917 AAGAGACAGCATGTGTGTTTACTCTCCAGAAAGACCTTCTCAAGAAACCACTCCAGA 976
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
 QY 977 ATACTTCCAGAAAACTTTGGCTCTGTAGAAGTCTAGCTCTCTTCATCCAGTAAGTTGATA 1036
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
 QY 1037 CCAGGGGTCCCACTTGTGTTTGTAGATAAACCTCAAGAAATTCAGATGTTTCATGAATTG 1096
 Db 341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360
 QY 1097 AGAGTAAACCGTTCTGTGTACAAAGATAAAAGAGACTCTCGAAGTGTCTTCTCAGACTG 1156

Db	361	ArgValIysArgSerValThrArgIleLysArgSerArgSerValPheTyrArgLeu	380
Qy	1157	ACCATACGTATATTAGTATTGTGTAGTTGGATGCACCTACACCTTTTCCATGTGGTA	1216
Db	381	ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal	400
Qy	1217	ACTGATTTTAAAGACAATCTTATTCAAATAGGCATTTCAAGTTGGTGTATTGCATTGTT	1276
Db	401	ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys	420
Qy	1277	CATTGTTGGCGATGATGCTCTGTGTCTTAATCAATTCATATGGTGGTTCTTAATAAT	1336
Db	421	HisLeuLeuGlyMetMetSerCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn	440
Qy	1337	GGGATTTAAAGCTGATTTAGTGTCCCTTATACACTGCTTTCATATG	1381
Db	441	GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet	455
RESULT 4			
AAW37093			
XX	ID	AAW37093 standard; protein; 455 AA.	
XX	AC	AAW37093;	
XX	DT	08-JUN-1998 (first entry)	
XX	XX	Homo sapiens hippocampal Y5 receptor.	
DE	XX	Hippocampal Y5 receptor; treatment; anorexia; bulimia; obesity;	
KW	KW	feeding behaviour; modification; atypical neuropeptide.	
KW	XX	Homo sapiens.	
OS	XX	W09746250-A1.	
XX	PN	11-DEC-1997.	
XX	PD	04-JUN-1997; 97WO-US009504.	
XX	PF	04-JUN-1996; 96US-00868650.	
XX	PR	21-FEB-1997; 97US-00803600.	
XX	PR	(SYNA-) SYNAPTIC PHARM CORP.	
XX	PA	Gerald CP, Weinehank RL, Walker MW, Brancheck T;	
PI	PI	WPI; 1998-051901/05.	
DR	DR	N-PSDB; AAV00622.	
XX	XX	DNA encoding canine hypothalamic atypical neuro:peptide Y/peptide YY	
PT	PT	receptor, Y5 - useful for identification of compounds which are capable	
PT	PT	of modifying feeding behaviour.	
XX	XX	Disclosure; Fig 6; 273pp; English.	
PS	PS	The sequence is that of a hippocampal Y5 receptor (Y5-R). Y5-r can be	
XX	CC	used in processes to determine whether a chemical compound specifically	
CC	CC	binds to and activates or inhibits a Y5-R by measuring a second messenger	
CC	CC	response. The chemical compounds can be used to increase or reduce the	
CC	CC	activity of a Y5-R. In particular, inhibitors can be used to treat	
CC	CC	obesity and activators can be used to treat anorexia. Antagonists capable	
CC	CC	of alleviating (by decreasing the activity of Y5-R) an abnormality can be	
CC	CC	identified by administering a potential antagonist to a transgenic mammal	
CC	CC	as above, and determining whether the substance alleviates the physical	
CC	CC	and behavioural abnormalities displayed by the transgenic mammal as a	
CC	CC	result of overactivity of a Y5-R. Agonists can be identified in a similar	
CC	CC	manner, but where the abnormality is alleviated by increasing the	
CC	CC	activity of Y5-R	
XX	XX	Sequence 455 AA;	

Pred. No.:	1,34e-253	Length:	455
Score:	2385.00	Matches:	455
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	96.17%	Indels:	0
DB:	2	Gaps:	0
US-09-771-956-4 (1-1406) x AA037093 (1-455)			
QY	17	ATGCTCTTTTATTCNAGCAGACTATATATATGGATTATAGACTCGACGAGTATTATAAC	76
Db	1	MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn	20
QY	77	AAGACACTTGCACACAGAAATAACTGCTGGCACTCGGAATTTCTGATTTCCAGAGCTGG	136
Db	21	LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr	40
QY	137	GATGACTATAAAGCAGTGTAGAGCTTACAGTATTTCTGATTTGGGCTCTATACATTT	196
Db	41	AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe	60
QY	197	GTAAGTCTTCTTGGCTTTATGGGGAATCTACTTATTTTAAATGGCTCTCATGAAAAAGCGT	256
Db	61	ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg	80
QY	257	AATCAGAAGACTACGGTAAACTTCCTCATAGGCAATCTGGCCCTTTCTGATATCTTGGTT	316
Db	81	AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal	100
QY	317	GTGCTGTTTGTCTACCTTTCACACTGAGCTGCTGCTGTGATCAGTGGATGTTTGGC	376
Db	101	ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTyrMetPheGly	120
QY	377	AAAAGTCATGTCATATTATGCTCTTTCTTCAATGTGTGTCAGTTTGGTTTCAACTTTA	436
Db	121	LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu	140
QY	437	ATTTTAAATCAATTGGCAATGTCAGGTATCATATGATTAAGCATCCCATCTCTAATAAT	496
Db	141	IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn	160
QY	497	TTAACAGCAAAACATGGCTACTTCTTGATAGTACTGCTGGACACTAGGTTTGGCATC	556
Db	161	LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle	180
QY	557	TGTTCTCCCTTCCAGTGTTTTCAGTCTTGTGGAACTTCAGAAACATTTGGTTTCAGCA	616
Db	181	CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla	200
QY	617	TTGCTGAGCAGCAGGTATTTATGTTTGGTTCATGGCCATCTGATTCATACAGAATTCGC	676
Db	201	LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla	220
QY	677	TTTACTATCTTTTATGTAGTTCAGTATATTTCTGCCCTTAGTTTCTTACTGTAAGT	736
Db	221	PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer	240
QY	737	CATCAGTGTCTGCAGAGTATAAGCTGTGGATTGTCCAAAGAAAAACAGACTTGAA	796
Db	241	HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu	260
QY	797	GAAAATCAGATGATCAACTTAACTCTTTCATCCATCCAAAAAGAGCTGGCCCTCAGGTAAA	856
Db	261	GluAsnGluMetIleAsnLeuThrLeuHisProSerLysSerGlyProGlnValLys	280
QY	857	CTCTCTGGCAGCATAATGGAGTATTCATTCATCAAAAACACAGAGAAGATATAGC	916
Db	281	LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer	300
QY	917	AAGAAGACAGCATGTGTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCTCCAGA	976
Db	301	LeuThrThrAlaCysValIleuProAlaProGluArgProSerGlnGluAsnHisSerArg	320

QY 977 ATACTCCAGAAAACCTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTGATA 1036
 |||||
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerSerLysPheLeu 340
 |||||
 QY 1037 CCAGGGGCCCCACCTTGTCTTGAGATAAAACCTGAGAAAATTCAGATGTTTCATGAATTG 1096
 |||||
 Db 341 ProGlyValProThrCysPheGluLeuLysProGluGluAsnSerAspValHisGluLeu 360
 |||||
 QY 1097 ACAGTAAACGGTCTCTTACAGAGATAAAAGAGATCTCGAAGTGTCTTACAGACTG 1156
 |||||
 Db 361 ArgValLysArgSerValThrArgGlyLysArgSerArgSerValPheTyrArgLeu 380
 |||||
 QY 1157 ACCATACATGATATTAGTATTGCTGTTAGTTGGATGCCACATACACCTTTCCATGTGGTA 1216
 |||||
 Db 381 ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
 |||||
 QY 1217 ACTGATTTTATGACAACTTATTTCATATAGGCAATTTCAAGTTGGTGTATTCGATTGT 1276
 |||||
 Db 401 ThrAspPheAsnAspAsnLeuLeuSerAsnArgHisPheLysLeuValTyrCysIleCys 420
 |||||
 QY 1277 CATTTGTTGGGCATGATGCTGCTGTTGCTTAATCCAAATTCATATGCGTTCCTTAATAAT 1336
 |||||
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
 |||||
 QY 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381
 |||||
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455
 |||||
 RESULT 5
 ID AAY57461
 XX standard; protein; 455 AA.
 AC AAY57461;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Human hippocampal Y5 receptor.
 XX
 KW Y5 receptor; feeding behaviour; food consumption; obesity; bulimia;
 KW anorexia; neuroleptic; genetic engineering.
 XX
 OS Homo sapiens.
 XX
 FN US968819-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 01-DEC-1995; 95US-00566096.
 XX
 PR 02-DEC-1994; 94US-00349025.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 FI Walker MW, Branchek T, Gerald CPG, Weinshank RL;
 XX
 DR WPI; 1999-590415/50.
 XX
 DR N-PSDB; AAZ339046.
 XX
 PT Nucleic acid encoding a human neuropeptide Y receptor useful in genetic
 PT engineering.
 XX
 PS Disclosure; Fig 6; 87pp; English.
 XX

CC The present sequence represents the human hippocampal Y5 receptor. The Y5
 CC receptor is a G-protein coupled neuropeptide Y receptor found throughout
 CC the mammalian nervous system and is a powerful stimulant of feeding
 CC behaviour. Cells expressing DNA encoding the Y5 receptor can be used to
 CC determine whether a ligand specifically binds to a Y5 receptor. These
 CC cells or a cell extract, is exposed to the ligand and then any binding
 CC between the ligand and the receptor can be detected. The cells can also
 CC be used to determine whether a ligand is a Y5 receptor antagonist or
 CC agonist. The binding of chemical compounds to a Y5 receptor can also
 CC determined and whether they activate or inhibit the activation of the Y5

CC receptor can also be determined using cells expressing the receptor. The
 CC effect of drugs on the Y5 receptor and whether they act as agonists or
 CC antagonists can also be detected with these cells
 XX
 SQ Sequence 455 AA;

Alignment Scores: 1 34e-253 Length: 455
 Pred. No.: 2385.00 Matches: 455
 Score: 2385.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x AAY57461 (1-455)

QY 17 ATGCTCTTTTATCCAGGAGCTATATATGGATTAGAGCTCGACGAGTATTATAAC 76
 |||||
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
 |||||
 QY 77 AAGACACTTGGCCACAGAGATAATATCTGCTGCTCCACTCGGAATTCGATTCCAGTCTGG 136
 |||||
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
 |||||
 QY 137 GATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTTCTGATTGGGCTCTATACATT 196
 |||||
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
 |||||
 QY 197 GTAAGTCTTCTGGCTTTATGGGGAATCTACTATTATTAATGGCTCTCATGAAAAGCGT 256
 |||||
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
 |||||
 QY 257 AATCAGAAGACTACGGTAAACTTCTCATAGCAATCTGGCTTTCTGATATCTTGGTT 316
 |||||
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
 |||||
 QY 317 GGTGCTGTTTGTCTACCTTTTCACACTGAGCTGTCTGCTGGATCAGTGGATTTGGC 376
 |||||
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
 |||||
 QY 377 AAGTCACTGTGCATATTATGCTTTTCTCAATGTGTGTCAGTCTTGGTTTCAACTTTA 436
 |||||
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 |||||
 QY 437 ATTTTAATATCAATGTCAGGTATCATATGATAAACAATCCCATATCTAATAAT 496
 |||||
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
 |||||
 QY 497 TTAACAGCAAAACCATGGCTACTTTCTGATAGTACTGTCTGGACACTAGGTTTGGCATC 556
 |||||
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
 |||||
 QY 557 TGTCTCCCTTCCAGTCTTTTCACAGTCTTCTGGAACCTCAAGAAACATTTGGTTCAGCA 616
 |||||
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200
 |||||
 QY 617 TTGCTGACGACGAGTATTATTATGTTGAGTCATGCGCCATCTGATTATACAGATTTGCC 676
 |||||
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
 |||||
 QY 677 TTTACTATCTCTTTTATTGCTAGTTAGTTATTTCTGCCCTTAGTTTGTCTTACTGTAGT 736
 |||||
 Db 221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
 |||||
 QY 737 CATCAAGTGTCTGCAGAGTATAGCTGTGGATTGTCCAAAGAAAGAAACAGACTTGAA 796
 |||||
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 |||||
 QY 797 GAAATGAGATGATCAACTTAACCTTCTCATCCATCCAAAAGAGTGGGCTCAGTCAAA 856
 |||||
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
 |||||
 QY 857 CTCTCGCCGCCATAAATGGAGTTATTCTATCTCAAAAACACAGAAAGATATAGC 916
 |||||

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Db      281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
QY      917 AAGAGACACATGTGTGTGTACCTGCTCCGAAAGACCTTCTCAAGAGAACCACTCCAGA 976
Db      301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
QY      977 ATACTTCCAGAAACATTGGCTCTGTAAAGAGTCAGCTCTCTTCATCCAGTAAGTTTCATA 1036
Db      321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
QY      1037 CCAGGGTCCCACTGCTTGTAGATAAAACCTGAAAGAAATTCAGATGTCATGAATG 1096
Db      341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360
QY      1097 AGAGTAAACGCTCTCTGTACAGATAAAAGAGATCTCGAAGTGTITTTCTACAGACTG 1156
Db      361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
QY      1157 ACATACTGATATAGTATTGCTGTGTAGTTGATGCCACTACACCTTTTCCATGTGTA 1216
Db      381 ThrIleLeuIleLeuValPheAlaValSerTyrMetProLeuHisLeuPheHisValVal 400
QY      1217 ACTGATTTTAAACACATCTTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCAATTTGT 1276
Db      401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY      1277 CATTTGTTGGCATGATGCTCTGCTGTTTAACTCAATTCATATAGGGTTCCTTAATAT 1336
Db      421 HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY      1337 GGGATTAAGCTGATTTAGTGTGCTTATACACTGCTTCATATG 1381
Db      441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 6
AAE08002
ID   AAE08002 standard; protein; 455 AA.
AC   AAE08002;
DT   01-NOV-2001 (first entry)
XX   Human neuropeptide Y5 (NPY5) receptor.
XX   Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
KW   transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW   Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW   locomotor; anxiety disorder; limbic seizure; tranquilliser; human.
OS   Homo sapiens.
FH   Key
FT   Domain
FT   1..50 Location/Qualifiers
FT   /note= "N-terminal extracellular domain"
FT   51..71
FT   /note= "First TM domain"
FT   72..84
FT   /note= "First intracellular loop domain"
FT   85..105
FT   /note= "Second TM domain"
FT   106..125
FT   /note= "First extracellular loop domain"
FT   126..145
FT   /note= "Third TM domain"
FT   147..167
FT   /note= "Second intracellular loop domain"
FT   168..188
FT   /note= "Fourth TM domain"
FT   189..220
FT   /note= "Second extracellular loop domain"
FT   221..241
FT   /note= "Fifth TM domain"

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FT   Domain
FT   242..378 /note= "Third intracellular loop domain"
FT   379..401
FT   /note= "Sixth TM domain"
FT   402..414
FT   /note= "Third extracellular loop domain"
FT   415..438
FT   /note= "Seventh TM domain"
FT   439..455
FT   /note= "C-terminal intracellular domain"
XX   W0200155103-A2.
XX   02-AUG-2001.
XX   29-JAN-2001; 2001WO-US002804.
XX   28-JAN-2000; 2000US-0178652P.
XX   (NEUR-) NEUROGEN CORP.
XX   Bennett M, Brodbeck R, Krause J;
XX   WPI; 2001-514543/56.
XX   N-PSDB; AAD14734.
XX   New chimeric receptor proteins comprising a single polypeptide chain of
XX   amino acids, useful as targets for drug actions, and as basis for drug
XX   discovery and development.
XX   Example 2; Page 55-56; 72pp; English.
XX   The present invention relates to chimeric neuropeptide Y (NPY) receptors.
XX   The NPY receptors are G-protein-coupled transmembrane proteins with seven
XX   membrane spanning transmembrane (TM) domains. The compounds that modulate
XX   the activity of a NPY receptor is useful in the preparation of a
XX   medicament for treating conditions including obesity, high/low blood
XX   pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
XX   seizure, locomotor and anxiety disorders. They can also be used as
XX   targets for drug actions, and as basis for drug discovery and
XX   development. The NPY5 receptor may have an anti-epileptic activity in the
XX   control of limbic seizures. The present sequence is human NPY5 receptor
XX   Sequence 455 AA;
SQ   Alignment Scores:
Pred. No.: 1,346-253 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: 4 Gaps: 0
US-09-771-956-4 (1-1406) x AAE08002 (1-455)
QY 17 ATGCTTTTATTCGAAGCAGGACTATATATGGATTTAGAGCTCGACGATATATAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTrpAsn 20
QY 77 AAGACACTTGGCCACAGAGATAATATCTGCTGCCACTCGGAATTTCTGATTTCCCACTCGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
QY 137 GATGACTATAAAGCAGTGTAGATGACTACAGTATTTTCTGATTTGGGCTCTATACATTT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAAGTCTTTCTGGCTTTATGGGAATCTACTATTTTAAATGGCTCTCATGAAAACGCT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAGACACTACGGTAAACTCTCTCATAGCAATCTGGCTTTCTGATATCTTGGT 316

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Best local Similarity: 100.00%
 Query Match: 96.17%
 DB: 5
 Mismatches: 0
 Indels: 0
 Gaps: 0
 US-09-771-956-4 (1-1406) x ABB84497 (1-455)

QY 17 ATGCTTTTATCCAGAGAGATATAATATGAGATTAGAGCTCGACAGTATTATAAC 76
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
 QY 77 AGACACTTGCACAGAGATATACTGCTGCACCTCGAATTCCTGATTTCCAGTCTGG 136
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
 QY 137 GATGACTATAAAGCAGTGTAGACTTACAGTATTTCTGATTGGCTCTATACATTT 196
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuLeuGlyLeuTyrThrPhe 60
 QY 197 GTAAGTCTTCTGGCTTATGCGGAATCTACTATTATTAATGGCTCTCATGAAAGCGT 256
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysArg 80
 QY 257 ATACAGAGACTACGGTAAACTCTCTCATAGCAATCTGGCTTTCTGTATATCTGGTT 316
 Db 81 AsnGlnLysThrThrValAsnPheLeuLeuGlyAsnLeuAlaPheSerAspLeuVal 100
 QY 317 GTGCTGTTTGTCTACCTTTCACACTGAGCTGTCTGCTGGATCAGTGCATCTTGGC 376
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
 QY 377 AAGTCATGTCATATTATGCTTTCTTCAATGTGTGTCAGTTTGGTTTCAACTTTA 436
 Db 121 LysValMetCysHisLeuMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 QY 437 ATTTAATATCAATGTCATGTCAGGATCATATGATAAACAATCCCATATCTAATAT 496
 Db 141 IleLeuLeuSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsn 160
 QY 497 TTAACAGCAACCATGGCTACTTTCTGATGACTGTCTGACACTAGTGTTCGCCATC 556
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuLeuAlaThrValTyrThrLeuGlyPheAlaIle 180
 QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAATCTCAAGAACTTCAAGAACTTGGTTCAGCA 616
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGlnThrPheGlySerAla 200
 QY 617 TTGCTGAGCAGCAGGTATTTATGCTTGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 676
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
 QY 677 TTACTATCTCTTTATGCTAGTTCAGTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 736
 Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
 QY 737 CATACAAAGTGTGTCAGAGTATAAGTGTGATTTGCTCAACAAAGAAAGAAAGAAAGTGA 796
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 QY 797 GAATGAGATCATCAATCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 856
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
 QY 857 CTCTCTGGCAGCCATAAATGGAGTTATTCATTCATCAAAAGAAAGAAAGAAAGATATAGC 916
 Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
 QY 917 AAGAGACAGCATGTGTTTACTCTCTCAGAAAGACCTTCTCAGAAAGACCTCAGCA 976
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
 QY 977 ATACTTCCAGAAATTTGGCTCTCTAAGAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1036
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340

QY 1037 CCAGGGTCCACCTGCTTTGAGATAAAACCTGAAGAAATTCAGATGTTTCATGAATTG 1096
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360
 QY 1097 AGAGTAAACGTTCTGTTTACAGATAAATAAAGAGATCTCGAAGTGTTCCTACAGACTG 1156
 Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
 QY 1157 ACCATGACTGATATTAGTATGCTGTTAGTTGGATGCGACTACACCTTTTCCATGTGGTA 1216
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
 QY 1217 ACTGATTTAATGACAACTTATTCAATAGGCAATTCAGTTGGTGTATGTGATTTGT 1276
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
 QY 1277 CATTTGTTGGGCATGATGCTGTTGCTTAACTTAATCAATTCATATGCTTCTTAATAAT 1336
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
 QY 1337 GGGATTAAGCTGATTTAGTGTCTTATACACTGCTTTCATATG 1381
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 8

ABB79510
 ID ABB79510 standard; protein; 455 AA.

AC ABB79510;
 DT 23-SEP-2002 (first entry)

XX Human neuropeptide Y5 receptor.
 DE XX
 XX Neuropeptide Y5; NPY; receptor; human; antagonist; anorectic;
 KW antiinflammatory; nootropic; neuroprotective; cardiovascular;
 KW hypotensive; antidiabetic; psychiatric; anticonvulsant; cardiac;
 KW cerebroprotective; antidepressant; haemostatic; tranquilizer;
 KW neuroleptic; analgesic; antianxiety; nephrotropic; uterine;
 KW gastrointestinal; antidiabetic.

XX Homo sapiens.

XX WC0200248152-A2.

XX 20-JUN-2002.

XX 11-DEC-2001; 2001WO-US047863.

XX 12-DEC-2000; 2000US-0254990P.

XX (NEUR-) NEUROGEN CORP.

XX Bakthavatchalam R, Blum CA, Brielmann HL, Darrow JW;
 De Lombaert S, Hutchison A, Tran J, Zheng X, Elliott RL, Hammond M;
 WPI: 2002-547845/58.
 N-PSDB; ABB84252.

XX New substituted spiro(isobenzofuran-1,4'-piperidin)-3-one or 3H-
 spiro(isobenzofuran-1,4'-piperidine, useful for treating, e.g. eating
 disorder, psychiatric, cardiovascular disorder or diabetes.

XX Example 675; Page 129-130; 134pp; English.

XX The present sequence is the protein sequence for the human neuropeptide
 Y5 (NPYs) receptor. In an example from the invention, chimeric receptors
 CC including human NPY5 receptor sequences were constructed, and used to
 CC assay the binding activity of compounds of the invention. Substituted
 CC spiro(isobenzofuran-1,4'-piperidin)-3-ones and 3H-spiro(isobenzofuran-1,4'-
 CC piperidines capable of modulating NPY5 receptor activity are provided.
 CC Such compounds may be used to modulate ligand binding to NPY5 receptors

CC in vivo or in vitro, and are particularly useful in the treatment of a
 CC variety of disorders, e.g. eating disorders such as obesity or bulimia,
 CC psychiatric disorders, diabetes and cardiovascular disorders such as
 CC hypertension, in humans and animals
 XX
 SQ Sequence 455 AA;

Alignment Scores:
 Pred. No.: 1.34e-253 Length: 455
 Score: 2385.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 5 Gaps: 0

US-09-771-956-4 (1-1406) x ABB79510 (1-455)

QY	17	ATGTCCTTTTATTC	CAAGCAGGACTATA	TATGATTTAGAGCTC	GAGCAGTATTATAAC	76
DB	1	MetSerPheTyrSer	LysGlnAspTyr	AsnMetAspLeu	GluLeuAspGluTyr	Asn 20
QY	77	AAGACACTTGCAC	AGAGATAATACTG	CTGCCACTCGGAAT	CTGATTTCCCACTCGG	136
DB	21	LysThrLeuAla	ThrGluAsnAsn	ThrAlaAlaThr	ArgAsnSerAspPhe	ProValTyr 40
QY	137	GATGACTATAAAG	CAGGTAGAGTAC	TACAGTATTTCTG	GATGGCTCTATACATTT	196
DB	41	AspAspTyrLys	SerSerValAsp	AspLeuGlnTyr	PheLeuIleGlyLeuTyr	Phe 60
QY	197	GTAAGTCTTCTG	CTTTATGGGAATC	TACTATTTTATG	TGGCTCTCATGAAAAAGCGT	256
DB	61	ValSerLeuLeu	GlyPheMetGly	AsnLeuLeuLeu	MetAlaLeuMetLysLys	Arg 80
QY	257	AATCAGAGACTAG	CGTAAACTTCTC	TATAGGCAATCTG	GCCTTTCTGATATCTTGTT	316
DB	81	AsnGlnLysThr	ValAsnPheLeu	IleGlyAsnLeu	AlaPheSerAspIleLeu	Val 100
QY	317	GTGCTGTTTGTG	CTCACACTGACG	CTCTCTTGTG	TGGATCAGTGGATGTTTGGC	376
DB	101	ValLeuPheCys	SerProPheThr	LeuThrSerVal	LeuLeuAspGlnTyrMetPhe	Gly 120
QY	377	AAAGTCATGCGCA	TATATGCCCTTT	TCTCAATGTGTG	TGTGCTTTGGTTTCAACTTTA	436
DB	121	LysValMetCys	HisIleMetPro	PheLeuGlnCys	ValSerValLeuValSerThr	Leu 140
QY	437	ATTTTAATATCA	ATTGCCATTTG	CAGGTATCATAT	GATATAAATCCATATCTATAAT	496
DB	141	IleLeuIleSer	IleAlaIleVal	ArgTyrHisMet	IleLysHisProIleSerAsn	Asn 160
QY	497	TTAACAGCAACCA	TGGCTACTTTCT	CATAGCTACTCTG	CTGGACACTAGGTTTGGCATC	556
DB	161	LeuThrAlaAsn	HisGlyTyrPhe	LeuIleAlaThr	ValTyrThrLeuGlyPheAla	Ile 180
QY	557	TGTTCTCCCTCC	AGGTTTTCAGN	CTTGTGGACTTC	CAAGAACATTTGCTTCAGCA	616
DB	181	CysSerProLeu	ProValPheHis	SerLeuValGlu	LeuGlnGluThrPheGlySer	Ala 200
QY	617	TTGCTGAGCAGC	AGGTTATTTATG	TGTGTTGAGTCA	TGCGCATCTGATTCATACAGAATG	676
DB	201	LeuLeuSerSer	ArgTyrLeuCys	ValGluSerTyr	ProSerAspSerTyrArgIle	Ala 220
QY	677	TTTACTATCTCT	TATGCTAGTTC	AGTATATTCG	CCCTTAGTTTGTCTTACTGTAAGT	736
DB	221	PheThrIleSer	LeuLeuValGln	TyrIleLeuPro	LeuValCysLeuThrValSer	240
QY	737	CATACAAAGTGT	CTGCAGAGTATA	AGCTGTGGATTG	TCCAAACAAAAACAGACTTGA	796
DB	241	HisThrSerVal	CysArgSerIle	SerCysGlyLeu	SerAsnLysGluAsnArgLeu	Glu 260
QY	797	GAATAATCAGAT	GATCAACTTACT	CTCTTCATCCAT	CCAAAAAGAGTGGGCTCAGGTGAAA	856
DB	261	GluAsnGluMet	IleAsnLeuThr	LeuHisPro	SerLysLysSerGlyProGlnVal	Lys 280

QY	857	CTCTCTGGCAGC	CAATAAATGGAG	TTATTTCATTCAT	CAAAAAACACAGAAAGATATAGC	916
DB	281	LeuSerGlySer	HisLysTyrSer	TyrSerPhe	IleLysHisArgArgTyrSer	300
QY	917	AAGAAGACACAT	GTGTGTACCTCT	CCAGAAAGACCTT	CTCAAGAGAACACACATCCAGA	976
DB	301	LysLysThrAla	CysValLeuPro	AlaProGluArg	ProSerGlnGluAsnHisSer	Arg 320
QY	977	ATACTTCCAGAA	AACTTTGGCTCT	GTGAAGAAGTCAG	CTCTTTCATCCAGTAAGTTCATA	1036
DB	321	IleLeuProGlu	AsnPheGlySer	ValArgSerGln	LeuSerSerSerLysPheIle	340
QY	1037	CCAGGGTCCCCA	CTTGTCTTGGAT	ATAAAACCTTGA	AGAAAAATTCAGATGTTTCATGAATG	1096
DB	341	ProGlyValPro	ThrCysPheGlu	IleLysProGlu	GluAsnSerAspValHisGluLeu	360
QY	1097	AGAGTAAACGTT	CTGTTCACAGAA	TAAAAAGAGATCT	CGAAGTGTCTTCTACAGACTG	1156
DB	361	ArgValLysArg	SerValThrArg	IleLysLysArg	SerArgSerValPheTyrArgLeu	380
QY	1157	ACCATACTCAT	ATTAGTATTGCT	GTAGTTGGATGCC	ACTACACCTTTTCCATCTGCTA	1216
DB	381	ThrIleLeuIle	LeuValPheAla	ValSerTyrMet	ProLeuHisPheHisValVal	400
QY	1217	ACTGATTTTAA	TGACAACTTAT	TTCAAATAGGCAT	TTTCAAGTTGGTGTATTCGATTGT	1276
DB	401	ThrAspPheAsn	AsnLeuIleSer	AsnArgHisPhe	LysLeuValTyrCysIleCys	420
QY	1277	CATTGTTGGCA	TGATGCTCTG	TCTTAAATCCAA	TTCTATATGGGTTTCTTAATAAT	1336
DB	421	HisLeuLeuGly	MetMetSerCys	CysLeuAsnPro	IleLeuTyrGlyPheLeuAsnAsn	440
QY	1337	GGGATTAAGCT	GATTAGTTAGT	GTCCCTTATAC	ACTGCTCTTCATATG 1381	
DB	441	GlyIleLysAla	AspLeuValSer	LeuIleHisCys	LeuHisMet 455	

RESULT 9

AAO23266	AAO23266	standard; protein; 455 AA.
ID	AAO23266	
XX	AAO23266;	
AC	AAO23266;	
XX	25-SEP-2003	(first entry)
DT	25-SEP-2003	
XX	Human neuropeptide Y5 receptor (NPY5) protein.	
DE	Neuropeptide Y5; receptor; NPY5; 2-cyclohexyl-4-phenyl-1H-imidazole; NPY;	
XX	appetite regulation; feeding disorder; obesity; bulimia; diabetes;	
KW	psychiatric; cardiovascular; hypertension; cerebral infarction; epilepsy;	
KW	schizophrenia; depression; angina; sudden cardiac death; vasospasm;	
KW	arrhythmia; urinary incontinence; Crohn's disease; asthma; neuroleptic;	
KW	antiinflammatory; nootropic; vasotropic; anticonvulsant; uropathic;	
KW	human.	

OS Homo sapiens.

XX EP1306085-A1.

XX 02-MAY-2003.

XX 21-OCT-2002; 2002EP-00023469.

XX 23-OCT-2001; 2001US-0348974P.

XX (NEUR-) NEUROGEN CORP.

XX Blum CA, Brielmann HL, De Lombaert S, Zheng X;

XX WPI; 2003-543553/52.

XX DR N-PSDB; AAL56583.

XX New 2-cyclohexyl-4-phenyl-1H-imidazole derivatives are modulators of
 PT neuropeptide Y5 receptor activity, useful for treating e.g. eating or

KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2004040000-A2.
 XX
 PD 13-MAY-2004.
 XX
 XX 09-SEP-2003; 2003WO-US028226.
 PF
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 XX (PRIM-) PRIMAL INC.
 PA
 XX
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX
 DR WPI; 2004-390329/36.
 DR N-PSDB; ADO30001.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 151; SEQ ID NO 666; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; calls derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 455 AA;

Alignment Scores:
 Pred. No.: 1,34e-253 Length: 455
 Score: 2385.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 8 Gaps: 0

US-09-771-956-4 (1-1406) x ADO29564 (1-455)

QY 17 ATGCTCTTTTATCCAGAGGACTATATATGATTAGAGCTCGACGAGTATATAAC 76
 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
 QY 77 AAGACACTTCCACAGAGAAATATATCTGCTGCCACTCGGAATCTGATTCTCCAGTCTGG 136
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
 QY 137 GATGACTATAAAGACAGTGTAGATGACTTACAGTATTTTCTGATGGGCTCTATCAATT 196
 Db 41 AspAspTyrLysSerSerValAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
 QY 197 GTAAAGTCTTCTGGCTTTATGGGAATCTACTATTATTTAATGGCTCTCATGAAAAGGCT 256
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysArg 80
 QY 257 ATCAGAGACTACGGTAAATCTCTCATAGCAATCTGGCCTTTTCTGATATCTTGTT 316
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
 QY 317 GTGCTGTTTGTCTACCTTTACACTGAGCTGCTGCTCTCGATCAGTGGATGTTGGC 376
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
 QY 377 AAGTCAATGCTCCATATTATGCTTTTCTTCAATGTGTGTCAGTTTGTGTTTCACTTTA 436
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 QY 437 ATTNTAATATCAATTGCCATCTGCTAGGTATCATATGATATAAACAATCCATATCAAT 496
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
 QY 497 TTAACAGCAAAACCATGGCTACTTTCTGATAGTACTGTCTGCACACTAGGTTTGGCCATC 556
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
 QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTACGA 616
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
 QY 617 TTGCTGAGCAGCAGTATTATGCTTTCAGTCATGGCCATCTGATTCATACAGAAATGCC 676
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
 QY 677 TTTACTATCTTTTATCTGATGTTTCTGATATATTCTGCCCTTGTGTTTGTCTTACTG 736
 Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
 QY 737 CATACAAGTGTCTCAGAGATATAGCTGTGATGTTCCACAAAGAGTGGGCTTCAGCTGAA 796
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 QY 797 GAAATGAGATGATCAACTTAACCTTTCATCCATCCAAAAGAGTGGGCTTCAGCTGAA 856
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
 QY 857 CTCCTGCGACCCATTAATGAGTATTTCATTCATCAAAAACACAGAGAGATATAGC 916
 Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
 QY 917 AAGAGACAGCATGTGTGTTTACCTGCTCCGAAAGACCTTCTCAAGAGAACCACTCCAGA 976
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
 QY 977 ATACTTCAGAAAATTTGGCTCTGTGAAGAGTCAAGTCTCTTCATCCAGTAAATTCATA 1036
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
 QY 1037 CCAGGGTCCCACTGCTTGTGAGATAAAACCTTGAAGAAAATTCAGATGTTTCATGAATTG 1096
 Db 341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360
 QY 1097 AGAGTAAACCTTCTGTTTCAAGAAATATAAAGAGATCTCGAAGTGTGTTTCTCAGACTG 1156

Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
 QY 1157 ACCATAGTATAGTATTGCTGTTAGTGGAGCCACTACACTTTTCCATGCGTA 1216
 Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
 QY 1217 ACTGATTTAAATGACAACTTATTTTCAAAATAGGCATTTCAAGTTGGTGTATTGCAATTTGT 1276
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
 QY 1277 CATTCTTGGGCGATGATGCTGCTCTTAATCCAAATCTATATGGGTTTCTTAATAT 1336
 Db 421 HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
 QY 1337 GGGATTAAGCTGATTAGTGTCCCTTATACACTGTCTTTCATATG 1381
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 11

AAE08016

ID AAE08016 standard; protein; 455 AA.

XX AC AAE08016;

XX 01-NOV-2001 (first entry)

XX African green monkey (AGM) neuropeptide Y5 (NPY5) receptor.

DE Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
 KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
 KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
 KW locomotor; anxiety disorder; limbic seizure; tranquilizer;
 KW African green monkey; AGM.

XX Cercopithecus aethiops.

XX W0200155103-A2.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US002804.

XX 28-JAN-2000; 2000US-0178652P.

XX (NEUR-) NEUROGEN CORP.

XX Bennett M, Brodbeck R, Krause J;

XX WPI; 2001-514543/56.

XX N-PSDB; AAD14746.

PT New chimeric receptor proteins comprising a single polypeptide chain of
 PT amino acids, useful as targets for drug actions, and as basis for drug
 PT discovery and development.

XX Example 2; Page 70-72; 72pp; English.

CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.
 CC The NPY receptors are G-protein-coupled transmembrane proteins with seven
 CC membrane spanning transmembrane (TM) domains. The compounds that modulate
 CC the activity of a NPY receptor is useful in the preparation of a
 CC medicament for treating conditions including obesity, high/low blood
 CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
 CC seizure, locomotor and anxiety disorders. They can also be used as
 CC targets for drug actions, and as basis for drug discovery and
 CC development. The NPY5 receptor may have an anti-epileptic activity in the
 CC control of limbic seizures. The present sequence is african green monkey
 CC (AGM) NPY5 receptor

XX Sequence 455 AA;

SQ Alignment Scores:

Pred. No.:	2,83e-252	Length:	455
Score:	2373.00	Matches:	452
Percent Similarity:	99.78%	Conservative:	2
Best Local Similarity:	99.34%	Mismatches:	1
Query Match:	95.69%	Indels:	0
DB:	4	Gaps:	0
US-09-771-956-4 (1-1406) x AAE08016 (1-455)			
QY 17	ATGCTCTTTTATCCAGCAGGACTATATATAGTATGATGGATTCGACGAGTATATAAC		76
Db 1	MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn		20
QY 77	AAGACACTTCCACACAGAGAATAATACTGCTGCCACTCGGAATTTCTGATTTCCCACTGCG		136
Db 21	LysThrLeuAlaThrGluAsnAsnThrAlaThrArgAsnSerAspPheProValTrp		40
QY 137	GATGACTATAAAGCAGGTAGATCACTACAGTATTTCTTCATGGCTCTCATACATTT		196
Db 41	AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe		60
QY 197	GTAAGTCTTTCTTGGCTTTATGGGAATCTACTTTATTTTAAATGGCTCTCATGAAAAGCGT		256
Db 61	ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg		80
QY 257	AATCAGAGACTACGGTAAACTTCCTCATAGGCATCTGGCCTTTCTGATATCTGGTT		316
Db 81	AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal		100
QY 317	GTGCTGTTTGTCTACCTTTTCCACTGACGCTGCTGCTGCTGGATCAGTGGATGTTGGC		376
Db 101	ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly		120
QY 377	AAAGTCATGTGCCATATTATGCCITTTCTTCAATGTGTGTCAGTTTGGTTCACCTTA		436
Db 121	LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu		140
QY 437	ATTTTAATATCAATTCCTCATTTGTCAGGTATCATATGATATAAACATCCCAVATCTAATAA		496
Db 141	IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn		160
QY 497	TTAAGCAGCAACCATGGCTACTTCTGATAGTACTGCTGGACACTAGGTTTGGCATC		556
Db 161	LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle		180
QY 557	TGTTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTCAGCA		616
Db 181	CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla		200
QY 617	TTGCTGACGACAGGTATTTATGTTGAGTCATGCGCATCTGATTCATACAGAAATGCC		676
Db 201	LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla		220
QY 677	TTTACTATCTCTTATTGCTAGTTTCAAGTATATCTGCGCTTAGTTTCTTACTGTAAGT		736
Db 221	PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer		240
QY 737	CATACAGTGTCTGACAGATATAGCTGTGGATGTCCACAAAGAAACAGACTTGAA		796
Db 241	HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu		260
QY 797	GAATAATGAGATCATCAACTTAACTCTTCATCCATCCAAAGAGCTGGGCTCAGGTGAA		856
Db 261	GluAsnGluMetIleAsnLeuThrLeuHisProSerArgLysIleGlyProGlnValLys		280
QY 857	CTCTCTGGCAGCCATAAATGAGTTATTCATTCATCAAAAACACAGAGAAGATATAGC		916
Db 281	LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer		300
QY 917	AAGAACAGCATGTGTGTATTACCTTCAGAAAGACTTCTCAAGAGAACCCTCCAGA		976
Db 301	LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg		320

QY 977 ATACTCCGAGAAACTTTGGCTGTGTAAGAGTACAGTCTCTTCATCCAGTAAGTTCATA 1036
 Db 321 IleLeuProGluAsnPhGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
 QY 1037 CCAGGGGTCCCACTTGTCTTTCAGATGAACTGAGAAATTCAGATGTTTCATGAATTG 1096
 Db 341 ProGlyValProThrCysPheGluLeuLysProGluGluAsnSerAspValHisGluLeu 360
 QY 1097 AGAGTAAACGCTTCTGTACAGAATAAAGAGATCTCGAAGTGTCTTCTACAGACTG 1156
 Db 361 ArgValLysArgSerValThrArgileLysLysArgSerArgSerValPheTyrArgLeu 380
 QY 1157 ACCATACATGATATTAGTATTCTGCTGTAGTGGATGCCACCTACACCTTTCCATGTCGTA 1216
 Db 381 ThrIleLeuIleuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
 QY 1217 ACTGATTTAATGACAATCTTATTTCAATAGGCAATTTCAAGTTGGTGTTATTCGATTGT 1276
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
 QY 1277 CATTTGTTGGGCATGATCTCTGTTGCTTCTTAATCCAAATCTATATGGTTCCTTAATAAT 1336
 Db 421 HisLeuLeuGlyMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
 QY 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGTCTTCATATG 1381
 Db 441 GlyIleLysAlaAspLeuMetSerLeuIleHisCysLeuHisMet 455

RESULT 12
 AAW27604
 ID AAW27604 standard; protein; 445 AA.
 AC AAW27604;
 DT 14-APR-1998 (first entry)
 DE Human neuropeptide Y receptor (NPY Y5).
 KW Neuropeptide Y receptor Y5; NPY Y5; peptide YY; NPY/Y receptor; human;
 KW neurotransmitter; antagonist; agonist; obesity; anorexia;
 KW hyperlipidaemia; diabetes; gene therapy; transgenic animal.
 OS Homo sapiens.
 PN W09737998-A2.
 PD 16-OCT-1997.
 PF 08-APR-1997; 97WO-US005781.
 PR 08-APR-1996; 96US-0014969P.
 PA (FARB) BAYER CORP.
 PI Hu Y, Mccaleb ML, Bloomquist BT, Flores-Riveros JR, Cornfield LJ;
 DR WPI; 1997-512637/47.
 DR N-PSDB; AAT73602.
 PT Nucleic acid molecule encoding neuro:peptide Y receptor - useful to
 PT identify antagonists and agonists, e.g. treat obesity, diabetes,
 PT hyperlipidaemia and anorexia.
 PS Claim 2; Page 37-39; 49pp; English.

CC antagonists could be used to treat obesity and diabetes by reducing
 CC appetite and food consumption, while agonists could be used to treat
 CC anorexia

XX SQ Sequence 445 AA;

Alignment Scores:
 Pred. No.: 1.56e-247 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x AAW27604 (1-445)

QY 47 ATGGATTAGAGCTCGACGAGTATTATAAAGACACTTGCACAGAGATAATATCTGCT 106
 Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
 QY 107 GCACCTCGGAATCTGATTTCCAGTCTGGGATGACTATAAAGCAGTGTAGATCACTTA 166
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
 QY 167 CAGTATTTCTGATTGGGCTCTATACATTGTAAAGTCTCTTGGCTTTATGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 QY 227 CTTATTTAATGGCTCTCATGAAAAAGCGTAAATCAGAAGACTACGGTAAACTTCCTCATA 286
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuIle 80
 QY 287 GGCATCTGGCCCTTTCTGATATCTTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGTCTTGTGTCAGTGGATGTTTGGCAAGTCATGTGCCATATATATGCTTTCTTCTT 406
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
 QY 407 CAATGTGTGTCAGTTTGGTTTCAACTTAAATTTAATCAATGCCATGTGTCAGTAT 466
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
 QY 467 CATATGATAAAACATCCCATATCTAATAATTAACAGCAAAACCATGGCTACTTCTGATA 526
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
 QY 527 GCTACTGTGTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 586
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
 QY 587 GTGGAATTCAGAAACATTTGGTTCAGCATTTGTCAGCAGCAGCAGCATTTATGTTGAG 646
 Db 181 ValGluLeuGlnLysThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
 QY 647 TCATGGCATCTGATTCATACAGAAATTCCTTTACTATCTCTTTATTGCTAGTTCAGTAT 706
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
 QY 707 ATTCTGCCCTTAGTGTGCTTACTGTAGTTCATCAAGTGTCTGACAGAGTATAGCTGT 766
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
 QY 767 GGATGTCCAAACAAAGAAACAGACTTGAAGAAATCAGATGATCAACTTAACTTCTCAT 826
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
 QY 827 CCATCCAAAAGAGTGGCCCTCAGTGAAACTCTCTGGCAGCCCATAAATGGAGTTATCA 886
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTrpSer 280
 QY 887 TTCATCAAAACACAGAAAGATATAGCAAGAACAGCATGTGTGTACCTGCTCCCA 946


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Db      261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
QY      887 TTTATCAAAACACACAGAGAGATATAGCAAGACAGCATGTGTGTTACTGCTCCA 946
Db      281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
QY      947 GAAAGACCTTCTCAAGAGACCACTCCAGATACTTCCAGAAACCTTGGCTCTGTAGA 1006
Db      301 GLUARGProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
QY      1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACACAGGGGTCCTGCTTTGAGATAAAA 1066
Db      321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
QY      1067 CTTGAACAAATTCAGATGTTTCATGATTCAGAGTAAGCGTCTGTTCACAGAAATAAAA 1126
Db      341 ProGluGluAsnSerAspValHISGluLeuArgValLysArgSerValThrArgIleLys 360
QY      1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATTAGTATTGCTGTAGT 1186
Db      361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer 380
QY      1187 TGAATGCCATACACCTTTCCATGCTGGTAACTGATTTTAATCACAATCTTATTTCAT 1246
Db      381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspLeuIleSerAsn 400
QY      1247 AGGCATTTCAAGTGTGTGTTATGCTATTGTCATTTGTTGGCATGATGCTGTTGCTT 1306
Db      401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLysLeu 420
QY      1307 AATCCAAATTCATATGGGTTCTTAAATATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366
Db      421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440
QY      1367 CACTGCTTTCATATG 1381
Db      441 HisCysLeuHisMet 445

RESULT 15
ID      AAY52578
XX      AA52578 standard; protein; 445 AA.
XX      AC      AAY52578;
XX      DT      28-FEB-2000 (first entry)
XX      DE      Human NPY (neuropeptide Y) Y5 receptor.
XX      KW      Neuropeptide Y; NPY; receptor; Y5; G-protein coupled; expression;
KW      chimeric; pharmacological property; peripheral nervous system;
KW      central nervous system; physiological; activity; food intake; feeding;
KW      thermogenesis; blood pressure; hormone release; gut motility;
KW      smooth muscle tone; sleep; circadian rhythm; neuronal excitability;
KW      nociception; mood; emotional response; seizure activity; diuresis;
KW      natriuresis; calciuresis; antisenescence; agonist; antagonist; obesity;
KW      hypertension; epilepsy; sexual dysfunction; jet lag.
XX
OS      Homo sapiens.
XX
XX      US5985616-A.
XX
PD      16-NOV-1999.
XX
PF      07-JAN-1998; 98US-00003199.
XX
PR      07-JAN-1998; 98US-00003199.
XX
PA      (SCHE ) SCHERING CORP.
XX
PI      Parker EM, Rudinski MS, Strader CD;
XX
XX      WPI; 2000-012792/01.
XX

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DR      N-PSDB; AAZ46232.
XX
PT      Chimeric mammalian neuropeptide Y5 receptor polypeptides useful for
PT      treating a range of disorders including jet lag, hypertension and sexual
PT      dysfunction.
XX
PS      Example; Col 37-40; 24pp; English.
XX
XX      This sequence represents human neuropeptide Y (NPY) Y5 receptor, cDNA
XX      encoding which was isolated and amplified from a human neuroblastoma cell
XX      line using primers AAZ46215-246223. The receptor was transiently
XX      expressed in COSI cells, but its level of expression was found to be
XX      significantly lower in comparison to that of the rat NPY Y5 receptor
XX      (AAY52579). The invention relates to a chimeric rat/human NPY receptor,
XX      comprising the 5' untranslated region (5' UTR) and extreme 5' coding
XX      region (105 bp) of the rat Y5 receptor cDNA, appended to nucleotides 365-
XX      1633 of the human Y5 receptor cDNA. When transfected into COSI cells, the
XX      chimeric construct yielded levels of expression higher than the native
XX      human Y5 receptor, and similar or greater levels of expression than the
XX      native rat Y5 receptor. The pharmacological properties of the chimeric
XX      receptor were similar to those of the native human Y5 receptor. NPY is
XX      widely distributed in both the peripheral and central nervous systems and
XX      has a wide range of physiological activities including effects on food
XX      intake, thermogenesis, blood pressure, hormone release, gut motility,
XX      smooth muscle tone, sleep and circadian rhythms, neuronal excitability,
XX      nociception, mood and emotional responses. NPY mediates these
XX      physiological effects via interactions with at least six distinct G-
XX      protein coupled receptors (designated Y1-Y6). The Y5 receptor mediates
XX      the effects of NPY on feeding, thermogenesis, neuronal excitability and
XX      seizure activity, diuresis, natriuresis and calciuresis. The chimeric Y5
XX      receptor, associated nucleic acids (e.g., expression vectors or antisense
XX      molecules), agonists or antagonists may be administered to treat
XX      disorders such as obesity, hypertension, epilepsy, sexual dysfunction and
XX      jet lag associated with abnormal expression/activity of NPY
XX
XX      Sequence 445 AA:
XX
XX      Alignment Scores:
XX      Pred. No.: 1,56e-247 Length: 445
XX      Score: 2330.00 Matches: 445
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 93.95% Indels: 0
XX      DB: 3 Gaps: 0
XX
XX      US-09-771-956-4 (1-1406) x AAY52578 (1-445)

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QY      47 ATGGATTATAGCTCGACGAGTATTATACAGACACATTCACAGAGATTAATCTGCT 106
Db      1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
QY      107 GCCACTCGCAATTCGATTTCCTCCAGTCTCGGATGACTATAAAGAGCAGTGTAGATGACTTA 166
Db      21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
QY      167 CAGTATTTCTGATGGGCTCTATACATTGTAAGTCTTCCTGGCTTTATGGGGAATCTA 226
Db      41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
QY      227 CTTATTTTAAATGGCTCTCATGAAGACGTAATCAGAAGACTACGCTAACTTCCTCAT 286
Db      61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80
QY      287 GGCAATCTGGCCCTTTCTGATATCTTGGTGTGCTGTTTTCCTCCTTCACACTGACG 346
Db      81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
QY      347 TCTGCTCTGCTGATCAGTGATGTTGGCAAGTGTGTCATGTCATATTATGCTTTCTT 406
Db      101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
QY      407 CAATGTGTGTCAGTGTGTTTTCACCTTAAATTAATATCAATTCGCTATTCAGGTAT 466

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Db 121 GlnCysValSerValLeuValSerThrLeuLeuLeuSerIleAlaIleValArgTyr 140
QY 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAAAACCATGGCTACTTTCTGATA 526
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
QY 527 GCTACTGTCGTGACACTAGGTTTCCCATCTGTTCCCTCCCTCCAGTGTTCACAGTCTT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerIleu 180
QY 587 GTGGAACCTTCAAGAAACATTTGGTTACGATGTGTGACAGCAGCATATTAATGTTGAG 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
QY 647 TCATGGCCATCTGATTCATACAGAAATGCCCTTACTATCTCTTATTGCTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
QY 707 ATTCTGCCCTTAGTTGCTTACTGTAGTCATACAAGTGTCTGCAGAAATATAAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
QY 767 GGATGTCTCAACAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACCTTCAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluAsnGluMetIleAsnLeuThrLeuHis 260
QY 827 CCATCCAAAAGAGTGGCCCTCAGGTGAACCTCTCTGGCAGCCATAAATGGAGTTATTCA 886
Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
QY 887 TTCATCAAAAACACAGAAAGATATAGCAAGAGACAGCATGTGTGTACCTGCTCCA 946
Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
QY 947 GAAAGACCTTCTCAAGAGAACCTCCAGAAATACTTCCAGAAACTTTGGCTCTGTAAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
QY 1007 AGTCAGTCTCTTCATCCAGTAAGTTCATACCCAGGGTCCCACTTGCTTTGAGATAAAA 1066
Db 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
QY 1067 CCTGAGGAATTCAGATGTTTCATGAATTCGAGTAAGCTTCTGTACAGAAATAAA 1126
Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
QY 1127 AAGAGATCTCGAGTGTGTTTCTACAGACTGACCATACTGATATTAGTATTGCTGTAGT 1186
Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer 380
QY 1187 TGGATGCCACTACACCTTTCCATGCTGGTAACGTATTTAATGACATCTTATTCAAAT 1246
Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400
QY 1247 AGGCATTTCAAGTTGGTGTATTGCTATTTGTCATTGTTGGCATGATGCTCTGCTGCTT 1306
Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420
QY 1307 AATCCAAATTCATATGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366
Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440
QY 1367 CACTGTCTTCATATG 1381
Db 441 HisCysLeuHisMet 445

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 21, 2004, 11:38:19 ; Search time 57 Seconds

(without alignments)
4746.694 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480

Sequence: 1 ttttggttgctgacaagtgt.....attctcaactgtttaccagaag 1406

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2/1/USPRO-spool_P/US09771956/runat_21102004_103737_9386/app_query.fasta_1.1543
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09771956@cgn 1 1 74 @runat_21102004_103737_9386 -NCPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481.5	19.4	366	2	neuropeptide Y/pep
2	481.5	19.4	384	2	neuropeptide Y/pep
3	480	19.4	349	2	G protein-coupled
4	480	19.4	382	2	neuropeptide Y/pep
5	480	19.4	382	2	neuropeptide Y/pep
6	464.5	18.7	375	2	pancreatic polypep
7	463.5	18.7	375	2	neuropeptide Y/pep
8	458	18.5	375	2	neuropeptide Y/pep
9	455.5	18.4	381	2	G protein-coupled
10	404	16.3	370	1	sulfakinin recepto
11	384	15.5	584	2	cholecystokinin-A
12	377	15.2	436	2	cholecystokinin-A
13	375	15.1	427	2	gastric CCK-A rece
14	368.5	14.9	444	2	cholecystokinin re

ALIGNMENTS

RESULT 1

S71152 neuropeptide Y/peptide YY receptor Y1 - African clawed frog

C;Species: Xenopus laevis (African clawed frog)

C;Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S71152; S55924

R;Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.

submitted to the EMBL Data Library, November 1993

A;Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenop

A;Reference number: S71152

A;Accession: S71152

A;Molecule type: mRNA

A;Residues: 1-366 <MAR>

A;Cross-references: UNIPROT:P34992; EMBL:L25416; NID:G409169; PIDN:AAA49918.1; PID:G4091

R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.

Biochim. Biophys. Acta 1261, 439-441, 1995

A;Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA f

A;Reference number: S55924; MUID:95260870; PMID:7742373

A;Accession: S55924

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-278, 'T', 280-366 <BLQ>

A;Cross-references: EMBL:L25416; NID:G409169

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Alignment Scores:

Pred. No.:	6.17e-35	Length:	366
Score:	481.50	Matches:	114
Percent Similarity:	43.75%	Conservative:	75
Best Local Similarity:	26.39%	Mismatches:	128
Query Match:	19.42%	Indels:	115
DB:	2	Gaps:	8

US-09-771-956-4 (1-1406) x S71152 (1-366)

Qy 71 TATNACAGACACTTGCACAGAGATAACTGCTGCCACTCGGAATTCGATTTCCTCA 130

15	367	14.8	449	2	A41738
16	356	14.4	428	2	UN0692
17	355.5	14.3	430	2	I51898
18	351.5	14.2	447	2	A47430
19	347	14.0	455	2	T15622
20	343.5	13.9	453	2	S2817
21	339.5	13.7	452	2	JC2459
22	329.5	13.3	450	2	JQ1614
23	329.5	13.3	452	2	A46195
24	320	12.9	423	2	B40470
25	316.5	12.8	457	2	T29741
26	309.5	12.5	423	2	JC7677
27	308.5	12.4	394	2	JC7209
28	306.5	12.4	365	2	T20184
29	303	12.2	399	2	T16277
30	302.5	12.2	398	1	JQ1059
31	302.5	12.2	412	2	T22076
32	300	12.1	443	2	D40470
33	295.5	11.9	374	2	T19340
34	294	11.9	349	2	I59336
35	293.5	11.8	390	2	B86694
36	293	11.8	391	2	T32714
37	288.5	11.6	357	2	JC7319
38	288.5	11.6	384	2	A41007
39	285	11.5	376	2	T19186
40	285	11.5	384	1	S00516
41	284	11.5	519	2	S17783
42	282.5	11.4	514	2	D56849
43	281.5	11.4	384	2	I57957
44	280.5	11.3	452	2	A34916
45	280.5	11.3	465	1	JQ1517

neuropeptide Y rec
cholecystokinin ty
cholecystokinin A
gastrin/cholecysto
hypothetical prote
gastrin receptor -
gastrin/cholecysto
gastrin receptor -
cholecystokinin B
glucocorticoid-ind
hypothetical prote
allatostatin recep
galanin receptor
hypothetical prote
hypothetical prote
neurokinin 2 recep
hypothetical-ind
glucocorticoid-ind
hypothetical prote
galanin receptor 1
protein AC7.1 [amp
hypothetical prote
probable allatosta
gastrin-releasing
hypothetical prote
neurokinin 2 recep
tachykinin recepto
dopamine receptor-
neurokinin 2 recep
neurokinin 3 recep
neurokinin 3 recep

Db 6 TyrPheGluAsnLeuSerValProAsnAsnIleSerGly-----AsnIleThrPhePro 23
 QY 131 GTCCTGGGATGACTATAAAGACAGTGTAGATGACATTTCTGATTTCTGATTTGGGCTC--- 187
 Db 24 IleSerGluAspCysAlaLeuProLeuPro-----MetIlePheThrLeuAlaLeuAla 41
 QY 188 TATACATTTGTAAAGCTCTTCTGGCTTTATGGGAATCTACTATTATTAAATGGCTCTCATG 247
 Db 42 TyrGlyAlaValIleIleLeuGlyLeuSerGlyAsnLeuAlaLeuIleIleLeu 61
 QY 248 AAAAGCGTATACAGAAGACTAGGTAACTCTCATAGGCAATCTGGCCCTTTTCTGAT 307
 Db 62 LysGlnLysGluMetArgAsnValThrAsnIleLeuIleValAsnLeuSerPheSerAsp 81
 QY 308 ATCTTGGTGTGCTGCTTTGCTCCTTTCACACTGACGCTGCTGCTGCTGATCAGTGG 367
 Db 82 LeuLeuAlaThrIleMetCysLeuProPheThrLeuIleIleThrLeuMetAspHisTirp 101
 QY 368 ATGTTTGGCAAGTCAATGCGCATATTATAGCTTTTCTCAATGCTGTCTGATTTTGGTT 427
 Db 102 IlePheGlyGluValMetCysLysLeuAsnGluTyrIleGlnCysValSerValThrVal 121
 QY 428 TCAACTTTAATTTAATATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
 Db 122 SerIlePheSerLeuValLeuIleAlaIleGluArgHisGlnLeuIleAlaAsnProArg 141
 QY 488 TCTAATAATTTAAACAGCAAAACCATGGCTTCTGATAGTACTGCTGACACTAGGT 547
 Db 142 GlyTyrArgProAsnAsnArgHisAlaCysPheGlyIleThrValIleTyrGlyPheAla 161
 QY 548 TTGTCATCTGTTCTCCCTCCAGTGTGTTTCCAGTGTGTTGGAACCTTCAGAAACATTT 607
 Db 162 MetAlaCysSerThrProLeuMetMetTyrSerValLeuThrAsp-----GluProPhe 179
 QY 608 GTTTCAGCATGCTGAGCAGC-----AGGTATTTATGTTGAGTGTGATGCTGCTGCT 658
 Db 180 LysAsnIleSerLeuAspSerTyrIleGlyLysTyrValCysLeuGluAspPheProGlu 199
 QY 659 GATTCATACAGATTCCTTACTCTCTTTATGCTGATGCTGATGCTGATGCTGCTGCTGCT 718
 Db 200 AspLysPheArgLeuSerThrThrThrLeuLeuPheIleLeuGlnTyrLeuGlyProLeu 219
 QY 719 GTTGTCTTACTGTAAAGTACAGAGTGTCTGCGAGAGTATAGCTGTGCTGCTGCTGCT 778
 Db 220 CysPheIlePheValCysTyrThrLysIle----- 229
 QY 779 AAAGAAACAGACTTGAAGAAATGAGATGATCACTTAACTTTCATCCATCCAAAAG 838
 Db 229 ----- 229
 QY 839 AGTGGGCTCAGTGAAACTCTCTGGCAGCCATAAATGGAGTATTTCATTCATCAAAAA 898
 Db 230 -----PheLeuArgLeu 233
 QY 899 CACAGAAGAAGATATAGCAGAGACAGACAGCATGTGTGTACTGCTGCCAAGAACCTTCT 958
 Db 234 LysArg----- 236
 QY 959 CAAGAGAACCACTCCAGAACTATCTCCAGAAAACTTGGCTGCTGTAGAACTGAGTCTCT 1018
 Db 236 ----- 236
 QY 1019 TCATCCAGTAGTTTCATACACAGGGGCTCCCACTGCTTTCAGATATAAACTGAGAAAT 1078
 Db 237 -----Asn 237
 QY 1079 TCAGATGTTCAATGATTCAGAGTAAACGTTCTGTTTCAAGAATAAAAAAGAGATCTCGA 1138
 Db 238 AsnMetMetAspLysIleArgAspAsnLysTyrArgSerSerGluThrLysArg----- 255
 QY 1139 AGTGTCTTACAGACTGACCATCTCATATTAGTATTCTGCTGCTGCTGCTGCTGCTGCT 1198

Db 256 ---IleAsnIleMetLeuLeuSerIleValValGlyPheAlaLeuCysTrpLeuProPhe 274
 QY 1199 CACCTTTTTCATGTGTAAGTCACTTTTAAATGACATCTTATTTCAATAGGATTTCAAG 1258
 Db 275 PheIlePheAsnLeuValPheAspTrpAsnHisGluAlaValAlaThrCysAsnHisAsn 294
 QY 1259 TTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1318
 Db 295 LeuLeuPheLeuIleCysHisLeuThrAlaMetIleSerThrCysValAsnProIlePhe 314
 QY 1319 TATGGTCTTCTTAATATGCGATTAAGCTGATTTA 1354
 Db 315 TyrGlyPheLeuAsnLysAsnPheGlnArgAspLeu 326
 RESULT 2
 A45490
 Neuropeptide Y/peptide YY receptor Y1 - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A45490; A46133; A42773
 R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
 J. Biol. Chem. 268, 6703-6707, 1993
 A:Title: Genomic organization, localization, and allelic differences in the gene for the
 A:Reference number: A45490; MUID:93203272; PMID:8095935
 A:Accession: A45490
 A:Molecule type: DNA
 A:Residues: 1-384 <HER>
 A:Note: sequence extracted from NCBI backbone (NCBI:128005; NCBI:128000)
 R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
 A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger
 A:Reference number: A46133; MUID:92283584; PMID:1321422
 A:Accession: A46133
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-384 <HE2>
 A:Note: sequence extracted from NCBI backbone (NCBI:108538)
 R:Arhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Foo, H.; Wahlested, C.
 J. Biol. Chem. 267, 10935-10938, 1992
 A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
 A:Reference number: A42773; MUID:92283782; PMID:1317848
 A:Accession: A42773
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-384 <LAR>
 A:Cross-references: GB:M88461; NID:g189155; PIDN:AAA73215.1; PID:g189156
 A:Experimental source: fetal brain
 A:Note: sequence extracted from NCBI backbone (NCBI:104735; NCBI:104736)
 C:Genetics:
 A:Gene: GDB:NPY1R; NPYR
 A:Cross-references: GDB:132643; OMIM:162641
 A:Map position: 4q31.3-4q32
 C:Superfamily: neurokinin 1 receptor
 F:37-66/Domain: transmembrane #status predicted <TM1>
 F:77-103/Domain: transmembrane #status predicted <TM2>
 F:118-136/Domain: transmembrane #status predicted <TM3>
 F:155-179/Domain: transmembrane #status predicted <TM4>
 F:209-232/Domain: transmembrane #status predicted <TM5>
 F:261-286/Domain: transmembrane #status predicted <TM6>
 F:300-323/Domain: transmembrane #status predicted <TM7>
 F:113-198/Disulfide bonds: #status predicted
 F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:338/Binding site: palmitate (Cys) (covalent) #status predicted
 Alignment Scores:
 Pred. No.: 6.18e-35 Length: 384
 Score: 481.50 Matches: 115
 Percent Similarity: 43.71% Conservative: 76
 Best Local Similarity: 26.32% Mismatches: 129
 Query Match: 19.42% Indels: 117
 DB: 2 Gaps: 8

US-09-771-956-4 (1-1406) x A45490 (1-384)

QY 74 AACAGACACTT-----GCCACAGAGATAATACTGCT-----GCCACTCG 115
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 Db 2 AsnSerThrLeuPheSerGlnValGluAsnHisSerValHisSerAsnPheSerGluLys 21
 |||||
 QY 116 AATCTGATTCCAGTCTGGATGACTATATAAGACAGGTAGATGACTACAGTATT 175
 |||||
 Db 22 AsnAlaGlnLeuLeuAlaPheGluAsnAspCysHisLeuProLeuAlaMetIlePhe 41
 |||||
 QY 176 CTGATTGGGTC--TATACATTGTGAAGTCTCTTGGCTTTATGGGGAATCTACTATT 232
 |||||
 Db 42 ThrLeuAlaLeuAlaTyrGlyAlaValIleIleLeuGlyValSerGlyAsnLeuAlaLeu 61
 |||||
 QY 233 TTAATGCTCTCATGAAAAAGCGTAATCAGAAGACTACGGTAACCTTCCTCATAGCAAT 292
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 Db 62 IleIleIleLeuLysGlnLysGluMetAsnValThrAsnIleLeuIleValAsn 81
 |||||
 QY 293 CTGCGCTTTCTGATCTTGGTGTGCTGCTGTTTGTCTCACTTTCACACTGACGTCTGTC 352
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 Db 82 LeuSerPheSerAspLeuLeuValAlaIleMetCysLeuProPheThrPheValTyrThr 101
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 QY 353 TTGCTGGATCAGTGGATGTTGGCAAGTCAATGTCATATTATGCTTTCTTCTCAATGT 412
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 Db 102 LeuMetAspHisTrpValPheGlyGluAlaMetCysLysLeuAsnProPheValGlnCys 121
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 QY 413 GTGTCAGTTTGGTTTCAACTTAAATTAATCAATTCGCTGTCAGGTATCATATG 472
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 Db 122 ValSerIleThrValSerIlePheSerLeuValLeuIleAlaValGluArgHisGlnLeu 141
 |||||
 QY 473 ATAAACATCCATCTAATAATTAACCAACCATGCTACTTCTGATAGTACT 532
 |||||
 Db 142 IleIleAsnProArgGlyTrpArgProAsnAsnArgHisAlaTyrValGlyIleAlaVal 161
 |||||
 QY 533 GTCTGGACACTAGTTTGGCTCTGCTCTCCCTTCAGTGTTCACAGTCTTGCGAA 592
 |||||
 Db 162 IleTrpValLeu-----AlaValAlaSerSerLeuProPheLeuIleTyrGlnValMet 179
 |||||
 QY 593 CTTCAGAAACATTTGGTTCAGCTTGTGAGCAGC-----AGTATTATGTT 643
 |||||
 Db 180 ThrAspGluProPheGlnAsnValThrLeuAspAlaTyrLysAspLysTyrValCysPhe 199
 |||||
 QY 644 GAGTCATGGCCATCTGATTCATACAGAAATGCCCTTTACTATCTCTTTATGCTAGTTCAG 703
 |||||
 Db 200 AspGlnPheProSerAspSerHisArgLeuSerTyrThrThrLeuLeuValLeuGln 219
 |||||
 QY 704 TATATTCTGCCCTTAGTTTGTCTTACTCTAGTCAATCAAGTGTCTGCAGAAAGTATAGC 763
 |||||
 Db 220 TyrPheGlyProLeuCysPheIlePheIleCysTyrPheLysIle----- 234
 |||||
 QY 764 TGTGATTGTCCACAAAGAAACAGACTTCAAGAAATGAGATGATCACTTAACCTT 823
 |||||
 Db 234 ----- 234
 QY 824 CATCATCAAAAAGAGTGGGCTCAGGTGAACCTCTTGGCAGCCATAATGAGTAT 883
 |||||
 Db 234 ----- 234
 QY 884 TCATTATCAAAAACACAGAGAGATATAGCAAGAACAGCATGTGTGTACCTGCT 943
 |||||
 Db 235 ---TyrIleArgLeuLysArgArg----- 241
 |||||
 QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCAGAAACCTTTGGCTCTGTA 1003
 |||||
 Db 241 ----- 241
 QY 1004 AGAAGTCAGCTCTCTTCATCCAGTAAGTTCATACCAGGGTCCCGCTTGTGAGATA 1063
 |||||
 Db 241 ----- 241
 QY 1064 AAACCTGAAGAAATTCAGATGTTTCATGAATTGAGAGTAAACGTTCTGTTACAGATA 1123
 |||||

Db 242 -----AsnAsnMetMetAspLysMetArgAspAsnLysTyrArgSerSerGlu 257
 QY 1124 AAAAGAGATCTGAGTGTCTTCTACAGACTGACCATCTGATATTAGTATTGCTGTT 1183
 |||||
 Db 258 ThrLysArg-----IleAsnIleMetLeuLeuSerIleValValAlaPheAlaVal 274
 |||||
 QY 1184 AGTTGGATGCCACTACACCTTTTCCATGTGGTAATGATTTTAAATGACAATCTTATTCA 1243
 |||||
 Db 275 CysTrpLeuProLeuThrIlePheAsnThrValPheAspTrpAsnHisGlnIleAla 294
 |||||
 QY 1244 AATAGGCATTCACAGTGTGATTCATTTGTCATTTGTTGGGCATGATGCTGTTGT 1303
 |||||
 Db 295 ThrCysAsnHisAsnLeuLeuPheLeuLeuCysHisLeuThrAlaMetIleSerThrCys 314
 |||||
 QY 1304 CTTAATCAATCTATATGTTGTTCTTAATATGGGATTAAGAGCTGATT 1354
 |||||
 Db 315 ValAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnArgAspLeu 331
 |||||

RESULT 3
 S12863
 A;protein-coupled receptor FC5 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
 C;Accession: S12863; S19101
 R;Eva, C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
 FEBS Lett. 271, 81-84, 1990
 A;Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the
 A;Reference number: S12863; MUID:91032093; PMID:2172008
 A;Accession: S12863
 A;Molecule type: mRNA
 A;Residues: 1-349 <EVA>
 A;Cross-references: UNIPROT:P21555; EMBL:Z11504
 R;Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
 submitted to the EMBL Data Library, November 1991
 A;Description: Pharmacological and Transduction Properties of a Recombinantly Expressed
 A;Reference number: S19101
 A;Accession: S19101
 A;Molecule type: mRNA
 A;Residues: 1-343; 'DDYTIAMSTVHTDVSKTSKQASPVPKFKISVMDNEKI' <KRA>
 A;Cross-references: EMBL:Z11504; NID:G57636; PIDN:CAA77579.1; PID:G57637
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
 F;39-61/Domain: transmembrane #status predicted <TM1>
 F;73-93/Domain: transmembrane #status predicted <TM3>
 F;114-135/Domain: transmembrane #status predicted <TM4>
 F;155-175/Domain: transmembrane #status predicted <TM5>
 F;213-231/Domain: transmembrane #status predicted <TM6>
 F;262-285/Domain: transmembrane #status predicted <TM7>
 F;299-322/Domain: transmembrane #status predicted <TM7>
 F;211.17/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;346/Binding site: phosphate (Thr) (covalent) #status predicted

Alignment scores:
 Pred. No.: 8,38e-35 Length: 349
 Score: 480.00 Matches: 114
 Percent Similarity: 42.63% Conservative: 74
 Best Local Similarity: 25.65% Mismatches: 127
 Query Match: 19.35% Indels: 126
 DB: 2 Gaps: 9

US-09-771-956-4 (1-1406) x S12863 (1-349)

QY 74 AACAGACACTT-----GCCACAGAGATAATACTGCT-----GCCACTCGAAT 118
 |||||
 Db 2 AsnSerThrLeuPheSerArgValGluAsnTyrSerValHisTyrAsnValSerGluAsn 21
 |||||
 QY 119 TCTGATTCCAGTCTGGGATGACTATAAAGCAGGTGTAGATGACTTACAGTATTTCTG 178
 |||||
 Db 22 SerProPheLeuAlaPheGluAsn-----AspAspCysHisLeuProLeu 36
 |||||
 QY 179 ATTGGGCTCTATACATT-----GTAACTCTTCTGCTTTATGGG 220
 |||||
 Db 37 AlaValIlePheThrLeuAlaLeuAlaTyrGlyAlaValIleLeuGlyValSerGly 56
 |||||

Db	177	IleLeuThrAsp-----GluProPheGlnAsnValSerLeuAlaAlaPheLysAspLys	194
Qy	632	TATTATGTGTAGTCATGCCATCTCATACAGAAATGCTTTTACTATCTCTTTA	691
Db	195	TyrValCysPheAspLysPheProSerAspSerHisArgLeuSerTyrThrLeuLeu	214
Qy	692	TTGCTAGTTCAAGTATTTCTGCCCTTAGTTTGTCTTACTTAAGTCATACAAAGTGTCTGC	751
Db	215	LeuValLeuGlnTyrPheGlyProLeuCysPheIlePheIleCysTyrPheLysIle---	233
Qy	752	AGAAATTAAGCTGTGGATTGTCCCAACAAAGAAACAGACTTGAAGAAATGAGATGATC	811
Db	233	-----	233
Qy	812	AACCTAACTCTTCATCCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCAT	871
Db	233	-----	233
Qy	872	AAATGGAGTTATTCATTCATCAAAAAACACAGAAAGATATAGCAAGAACAGCATGT	931
Db	234	-----TyrIleArgLeuLysArgArgAsnAsnMetMetAspLys-----	246
Qy	932	GTGTTACCTGCCAGAAAGACTTCTCAAGAGAACCACTCCAGAAATACTTCCAGAAAAC	991
Db	246	-----	246
Qy	992	TTTGCTCTGTGAAGAGTCAGCTCTCTTCATCCAGTAAGTTCAACACAGGGTCCCCACT	1051
Db	247	-----IleArgAspSerLysTyrArgSerSerGlu-----	256
Qy	1052	TGCTTTGAGATAAAACCTGAAAGAAATTCAGATGTTTCATGAATTGAGAGTAAACGTTCT	1111
Db	256	-----	256
Qy	1112	GTTACAGAAATAAAAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATTA	1171
Db	257	-----ThrLysArgIleAsnValMetLeuLeuSerIleValVal	269
Qy	1172	GTATTGTGTGTAGTGGATCCACTACACCTATTTCCATGTGTGTAACCTGATTTTAAATGAC	1231
Db	270	AlaPheAlaValCysTyrLeuProLeuThrIlePheAsnThrValPheAspTyrAsnHis	289
Qy	1232	AATCTATTCAATAGGCATTTCAAGTTGGTGTATTCATTTGTCATTTGTTGGGCATG	1291
Db	290	GlnIleIleAlaThrCysAsnHisAsnLeuLeuPheLeuLeuCysHisLeuThrAlaMet	309
Qy	1292	ATGTCCTGTGTCTTAATCCAAATCTATATGGGTTTCTTAATAATGGGATTAAGCTGAT	1351
Db	310	IleSerThrCysValAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnArgAsp	329
Qy	1352	TTA 1354	
Db	330	Leu 330	
RESULT 5			
S27388			
neuropeptide Y receptor NPY-1 - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004			
C:Accession: S27388			
R:Evans, C.; Oberto, A.; Sprengel, R.; Genazzani, E.			
FEBS Lett. 314, 285-288, 1992			
A:Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex			
A:Reference number: S27388; MUID:93106169; PMID:1468559			
A:Accession: S27388			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-382 <EVA>			
A:Cross-references: UNIPROT:Q04573; EMBL:Z18280; NID:G53438; PIDN:CAA79157.1; PID:G53439			
C:Superfamily: neurokinin 1 receptor			
Alignment Scores:			

Pred. No.:	8,41e-35	Length:	382
Score:	480.00	Matches:	114
Percent Similarity:	42.86%	Conservative:	75
Best Local Similarity:	25.85%	Mismatches:	126
Query Match:	19.35%	Indels:	126
DB:	2	Gaps:	9
US-09-771-956-4 (1-1406) x S27388 (1-382)			
Qy	74	AAACAGACACTT-----GCCACAGAGATAATACTGCT-----GCCACTCGGAAT	118
Db	2	AsnSerThrLeuPheSerLysValGluAsnHisSerIleHisTyrAsnAlaSerGluAsn	21
Qy	119	TCTGATTTCCCACTGCTGGGATGACTATAAAGCAGCTAGTAGTACTTACAGATTTTCTG	178
Db	22	SerProLeuAlaPheGluAsn-----AspAspCysHisLeuProLeu	36
Qy	179	ATTGGGCTCTATACATT-----GTAAGTCTTCTGGCTTTATGGG	220
Db	37	AlaValIlePheThrLeuAlaLeuAlaTyrGlyAlaValIleIleLeuGlyValSerGly	56
Qy	221	AATCTACTTATTTTATGCTCTCATGAAAAAGCGTAATCAGAAGACTACGGTAACATTC	280
Db	57	AsnLeuAlaLeuIleIleIleLeuLysGlnLysGluMetArgAsnValThrAsnIle	76
Qy	281	CTCATAGGCAATCTGGCCTTTCTGATATCTTGGTTGCTGCTGTTTTCCTCACCCTTCA	340
Db	77	LeuIleValAsnLeuSerPheSerAspLeuLeuValAlaValMetCysLeuProPheThr	96
Qy	341	CTGACGCTGCTGCTGCTGGATCAGTGGATGTTGGTGGTGGTGGTGGTGGTGGTGGT	400
Db	97	PheValTyrThrLeuMetAspHisTyrValPheGlyGluThrMetCysLysLeuAsnPro	116
Qy	401	TTTCTTCAATGTGTGTCAGTTTGGTTTCAACTTTTAAATTTTAAATATCAATATGCCATT	460
Db	117	PheValGlnCysValSerIleThrValSerIlePheSerLeuValLeuIleAlaValGlu	136
Qy	461	AGTATCATCATGATAAAACATCCATATCTAATAATTTTAAACAGCAACCATGCTACT	520
Db	137	ArgHisGlnLeuIleIleAsnProArgGlyTyrArgProAsnAsnArgHisAlaTyrIle	156
Qy	521	CTCATAGTACTGCTGCGACACTAGGTTTGGCATCTGTTCTCTCCCTTCCAGCTGTTT	580
Db	157	GlyIleThrValIleTyrValLeuAlaValAlaSerSerLeuProPheValIleTyrGln	176
Qy	581	AGTCTTGTGGAATCTCAAGAACATTTGTTTCCAGCATTCCTGAGCAGC-----AGG	631
Db	177	IleLeuThrAsp-----GluProPheGlnAsnValSerLeuAlaAlaPheLysAspLys	194
Qy	632	TATTTATGCTTGTGAGTCATGGCCATCTGATTTCATACAGAAATGCGCTTTACTATCT	691
Db	195	TyrValCysPheAspLysPheProSerAspSerHisArgLeuSerTyrThrThrLeuLeu	214
Qy	692	TTGCTAGTTCAAGTATTTCTGCCCTTAGTTTGTCTTACTTAAGTATCAAGTGTCTGC	751
Db	215	LeuValLeuGlnTyrPheGlyProLeuCysPheIlePheIleCysTyrPheLysIle---	233
Qy	752	AGAAGTATAAGCTGTGGAATTTGCCAACAAAGAAACAGACTTGAAGAAATGAGATGATC	811
Db	233	-----	233
Qy	812	AACCTAACTCTTCATCCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCAT	871
Db	233	-----	233
Qy	872	AAATGGAGTTATTCATTCATCAAAAAACACAGAAAGATATAGCAAGAACAGCATGT	931
Db	234	-----TyrIleArgLeuLysArgArgAsnAsnMetMetAspLys-----	246
Qy	932	GTGTTACCTGCCAGAAAGACTTCTCAAGAGAACCACTCCAGAAATACTTCCAGAAAAC	991
Db	246	-----	246

R; Yan, H.; Yang, J.; Marasco, J.; Yanaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.
submitted to the EMBL Data Library, December 1995
A; Reference number: H01018
A; Accession: G02300
A; A; A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-375 <YAN>
A; A; Cross-references: UNIPROT: P50391; EMBL: U42387; NID: g13.44327; PIDN: AAB07759.1; PID: G
C; Superfamily: neurokinin 1 receptor

Alignment Scores:	
Pred. NO.:	2.52e-33
Score:	463.50
Percent Similarity:	42.96%
Best Local Similarity:	25.12%
Query Match:	18.69%
DB:	2
Length:	375
Matches:	102
Conservative:	72
Mismatches:	121
Indels:	111
Gaps:	6

US-09-771-956-4 (1-1406) x G02300 (1-375)

[illegible]

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Db      262 ----- 262
QY      989 AACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTCATACGGGGTCCCC 104
Db      262 ----- 262
QY      1049 ACTTGCTTTGAGATAAAACCTGGAAGAAATTCAGATGTTTCATGAATTGAGAGTAAACGT 1108
Db      262 ----- 262
QY      1109 TCTGTTACAAGATAAAAAAGAGATCTCGAAGTGTTTCTACAGACTGACCATCTGATA 1168
Db      263 -----ValAsnValIleuValMetVal 271
QY      1169 TTAGTATTGCTGTAGTTGGATGCCACTACACTTTTCCATGTGCTAACTCATTTTAAAT 1228
Db      272 ValAlaPheAlaValLeuTrpLeuPheAsnSerIleuGluAspTrpHis 291
QY      1229 GACAATCTTATTCAAATAGGCATTTCACAGTTGGTGCTATTGTCATTGTTCATTGTGGGC 1288
Db      292 HisGluAlaIleProIleCysHisGlyAsnLeuIlePheLeuValCysHisLeuLeuAla 311
QY      1289 ATGATGTCCTCTGTCCTTAATCAATTCATATATGGGTTTCTTAATAATGGGATTAAAGCT 1348
Db      312 MetAlaSerThrCysValAsnProPheIleTyrGlyPheLeuAsnThrAsnPhenyls 331
QY      1349 GATTAGTGTCCCTTATA 1366
Db      332 GluIleLysAlaLeuVal 337

RESULT 8
S63685
neuropeptide Y receptor D type - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S63685
R:Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, R.S.; Lett, S.L., 58-62, 1996
A:Title: Cloning and characterization of a novel receptor to pancreatic polypeptide
A:Reference number: S63685; MUID:96193913; PMID:8641440
A:Accession: S63685
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-375 <GRE>
A:Cross-references: UNIPROT:Q61041; EMBL:U40189; NID:G1223969; PIDN:AAC52442.1
C:Superfamily: neurokinin 1 receptor

```

Alignment Scores:	
Pred. No.:	7.83e-33
Score:	458.00
Length:	375
Matches:	105
Conservative:	65
Mismatches:	120
Indels:	138
Gaps:	7
Percent Similarity:	40.67%
Best Local Similarity:	25.12%
Query Match:	18.47%
DB:	2

US-09-771-956-4 (1-1406) x S63685 (1-375)

QY	161	GACTTACAGTATTTCGTAGTTGGGCTCATACATTTGTAAAGTCTCTTGGCTTTATGGG	220
		: : : : : : :	
Db	39	GluLeuLeuAlaPheIleIleThrThrThrSerIleGluThrIleLeuGlyValLeuGly	58
		: : : : : : :	
QY	221	AATCTACTATTATTAAAGGCTCTCATGAAACCGTAATACAGAGACTACGGTAACTTC	280
		: : : : : : :	
Db	59	AsnLeuCysLeuIlePheValThrThrArgGlnLysGluLysSerAsnValThrAsnLeu	78
		: : : : : : :	
QY	281	CTCATAGCAATCTGGGCTTTTCTGATATCTCGTGTGCTGTGTTCACCTTTACA	340
		: : : : : : :	
Db	79	LeuIleAlaAsnLeuAlaPheSerAspPheLeuMetCysLeuIleCysGlnProLeuThr	98
		: : : : : : :	
QY	341	CTGAGCTGTGCTGTGGGATCAGTGGATGATTTGGCAAGTCATGTGCCATATATAGCT	400
		: : : : : : :	
Db	99	ValThrThrIleMetAspTyrTpIlePheGlyGluValLeuCysLysMetLeuThr	118
		: : : : : : :	

QY 401 TTCTTCAATGCTGTCAGCTTTGGTTTCACTTTAAATTTTAAATCAATGCCATGTC 460
 Db 119 PheileGlnCysMetSerValThrValSerLeuLeuValAlaLeuGlu 138
 QY 461 AGTATCATATGATAAACAATCCATATCTAATAATTTAACAACAACCATGGCTACTTT 520
 Db 139 ArgHisGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 158
 QY 521 CTGATAGTACTGCTGGACACTAGGTTTGGCCATCTGTTCTCCCTT----- 568
 Db 159 GlyLeuValValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 178
 QY 569 -----CCAGTGTTCAC-----AGTCTGTGGAACTTCAAGAAACATTT 607
 Db 179 ThrLeuAsnAspLeuPheHisTyrAsnHisSerLysValValGlu----- 193
 QY 608 GGTTCAGCATCTGTCAGCAGCAGGATTTATGTTGTGATGATGATGATGATGATGAT 667
 Db 194 -----PheLeuGluAspLysValValCysPheValSerTrpSerAspHisHis 210
 QY 668 AGAATGCTTTACTATCTCTTTATGCTAGTGTAGTATATTCGCCCTTGTGTTGCTT 727
 Db 211 ArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 230
 QY 728 ACTGTAAGTCATACAAGTGTCTGCAGAAAGTATAAGCTGTGGATGTTCCACAAAGAAAC 787
 Db 231 LeuValCysTyrIleArgGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 241
 QY 788 AGACTTGAAGAAATGAGATGATCAACTTAATCTTTCATCCATCCAAAGAGTGGCCT 847
 Db 241 ----- 241
 QY 848 CAGGTGAACCTCTCGGCAGCATAAATGGAGTATTATTCAATCAACAAACACAGAGA 907
 Db 241 ----- 241
 QY 908 AGATATGACAAAGACAGCATGTGTGTACCTGCTCAGAAAGACCTTCTCAAGAGAAC 967
 Db 242 -----GlnArgGlnLysHisValPhe 248
 QY 968 CACTCCGAATACTTCCAGAAACCTTGGCTCTGTAGAGAGTCTCTTCAATCCAGT 1027
 Db 249 HisAlaHisAlaCysSerSerArgAlaGlyGlnMet----- 260
 QY 1028 AAGTTTCAACAGGGGTCCCACTTCTGTTGAGATAAAACCTGAAGAAATTCAGATGTT 1087
 Db 260 ----- 260
 QY 1088 CATGAATGAGAGTAAACGTTCTGTACAGAAATAAAAGAGATCTCGAAGTGTTC 1147
 Db 261 -----LysArgIleAsnSerMet--- 266
 QY 1148 TACAGACTGACCACTACTGATATTAGTATTGCTGTAGTGGATGCCACTACACCTTTTC 1207
 Db 267 -----LeuMetThrMetValThrAlaPheAlaValLeuTrpLeuProLeuHisValPhe 284
 QY 1208 CATGTGTAATGATTTTAAATGACATCTTATTCAATAGGCAATTCAGTGTGGTAT 1267
 Db 285 AsnThrLeuGluAspTrpTyrGlnGluAlaIleProAlaCysHisGlyAsnLeuIlePhe 304
 QY 1268 TGCATTGTGATTTGTTGGCATGATCTGCTGTCTTAATCAATCTATATGTTGTTT 1327
 Db 305 LeuMetCysHisLeuLeuAlaMetAlaSerThrCysValAsnProPheIleTyrGlyPhe 324
 QY 1328 CTTAATATGGGATTAAGCTGATTTAGTGTCCCTTATA-----CACTGT 1372
 Db 325 LeuAsnIleAsnPheLysLysAspIleLysAlaLeuValLeuThrCysHisCys 342

RESULT 9

neuropeptide Y receptor Y2 - human

N; Alternate names: neuropeptide Y/peptide YY receptor type 2
 139187

C; Species: Homo sapiens (man)
 C; Date: 01-Mar-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
 C; Accession: I39187; I39163; G02301
 R; Gerald, C.; Walker, M.W.; Vayssie, P.J.
 J. Biol. Chem. 270, 26758-26761, 1995
 A; Title: Expression cloning and pharmacological characterization of a human hippocampal
 A; Reference number: I39187; MUID:96070760; PMID:7592910
 A; Status: preliminary
 A; Accession: I39187
 A; Molecule type: mRNA
 A; Residues: 1-381 <R0S>
 A; Cross-references: UNIPROT:P49146; EMBL:U36269; NID:G1063633; PID:AA050281.1; PID:G1063
 R; Rose, P.M.; Ferrandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kier
 J. Biol. Chem. 270, 22661-22664, 1995
 A; Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptide
 A; Reference number: I39163; MUID:96032678; PMID:7559383
 A; Accession: I39163
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-133, 'A', 135-381 <R0S>
 A; Cross-references: EMBL:U32500; NID:G1000750; PID:AAA93170.1; PID:G1000751
 R; Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.
 Submitted to the EMBL Data Library, December 1995
 A; Reference number: H01019
 A; Accession: G02301
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-171, 'G', 173, 'R', 175-201, 'P', 203-208, 'A', 210-381 <YAN>
 A; Cross-references: EMBL:U42389; NID:G1314329; PID:AA0760.1; PID:G1314330
 C; Genetics:
 A; Gene: GDB:NPY2R
 A; Cross-references: GDB:4365607; OMIM:162642
 A; Map position: 4q31-4q31
 C; Superfamily: neurokinin 1 receptor
 C; Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
 F; 49-76/Domain: transmembrane #status predicted <TM1>
 F; 87-113/Domain: transmembrane #status predicted <TM2>
 F; 166-186/Domain: transmembrane #status predicted <TM4>
 F; 221-237/Domain: transmembrane #status predicted <TM5>
 F; 269-291/Domain: transmembrane #status predicted <TM6>
 F; 305-328/Domain: transmembrane #status predicted <TM7>
 F; 123-203/Disulfide bonds: #status predicted
 F; 342/Binding site: palmitate (Cys) (covalent) #status predicted
 F; 372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 1,318-32 Length: 381
 Score: 455.50 Matches: 104
 Percent Similarity: 43.03% Conservative: 72
 Best Local Similarity: 25.43% Mismatches: 114
 Query Match: 18.37% Indels: 119
 DB: 2 Gaps: 9

US-09-771-956-4 (1-1406) x I39187 (1-381)

QY 161 GACTTACAGTATTTCTGATGGGCTCTATACATTTGTAGTCTTCTGGTGTATGCGG 220
 Db 48 GluValGlnValValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 67
 QY 221 AATCTACTATTTTAAATGGCTCTCATGAAAAGCGTAATCAGAACTACGGTAAATTC 280
 Db 68 AsnSerLeuValIleHisValValIleLysPheLysSerMetArgThrValThrAspPhe 87
 QY 281 CTCATAGCAATCTGGCCCTTTCTGATATCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 340
 Db 88 PheIleAlaAsnLeuAlaValAlaAspLeuLeuValAsnThrLeuLeuLeuLeuLeuLeu 107
 QY 341 CTGAGCTCTGCTTCTGCGGATGATGTTTGGCAAGTCATGTCATATATGCTT 400
 Db 108 LeuThrTyrThrLeuMetGlyGlyTrpLysMetGlyProValLeuLeuLeuLeuLeuLeu 127
 QY 401 TTTCTTCAATGTGTGTCAGTGTGTTTCACTTTTAAATTTTAAATATCAATTCGCAATGTC 460
 Db 401 TTTCTTCAATGTGTGTCAGTGTGTTTCACTTTTAAATTTTAAATATCAATTCGCAATGTC 460

Db 128 TyrAlaGlnGlyLeuAlaValGlnValSerThrIleThrLeuThrValIleAlaLeuAsp 147
Qy 461 AGTATCATATGATAAAACATCCCATATCTAATAATTAACAGCAACCATGCTACTTT 520
Db 148 ArgHisArgCysIleValTyrHisLeuGluSerLysIleSerLysArgIleSerPheLeu 167
Qy 521 CTGATAGCTACTGCTCGACACATAGGTTTGGCCATCTGTTCTCCCTTCCAGTGT--- 577
Db 168 IleIleGlyLeuAlaTrpGlyIleSerAlaLeuLeuAlaSerProLeuAlaIlePheArg 187
Qy 578 ---CACAGTCTTGGAGACTTCAAGAAACATTTGGTTCAGCATTTGCTGACAGCAGGTAT 634
Db 188 GluTyrSerLeuIleGluIleProAspPhe-----GluIleVal 201
Qy 635 TTATGTTGTCAGTCATCGGCATCTGATCA-----TACAGAAATGCTTTACTATC 685
Db 202 AlaCysThrGluLysTrpProGlyGluGlySerIleTyrGlyThrValTyrSerLeu 221
Qy 686 TCTTTATTGCTAGTACGTATTAITCTGCCCTTAGTTTGTCTTACTGTAAGTCATACAGT 745
Db 222 SerSerLeuLeuIleLeuTyrValLeuProLeuGlyIleIleSerPheSerTyrThrArg 241
Qy 746 GCTGTCAGAGTATAAGCTGTGGATTGTCCACAAAGAACACAGACTTGAAGAAATGAG 805
Db 242 Ile----- 242
Qy 806 ATGATCAACTTAACCTTTCATCCATCCAAAGAGTGGGCTCAGGTGAAACTCTCTGGC 865
Db 242 ----- 242
Qy 866 AGCCATAATCGAGTTATTCATTATCAACAAACACAGAGAGATATAGCAGAGACA 925
Db 243 -----TrpSer----- 244
Qy 926 GCATGTGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGATACTTCCA 985
Db 245 -----LysLeuLysAsnHis----- 249
Qy 986 GAAAACTTTGGCTCTGTAAGAAGTCAGCTCTTTCATCCAGTAAAGTTCATACAGGGGTC 1045
Db 250 -----ValSerProGlyAla 254
Qy 1046 CCCACTTGTGAGATAAAACCTGAGAAATTCAGATGTTTCATGAATTCAGAGTAAAA 1105
Db 255 -----AlaAsnAspHisTyrHisGlnArgArgGlnLys 265
Qy 1106 GCTTCTGTTTCAAGAAATAAAAGAGATCTCGAAGTGTCTTCTACAGACTGACCATACTG 1165
Db 266 -----ThrThrLysMet-----LeuValCysVal 273
Qy 1166 ATATTAGTATTGCTGTGTTAGTGGATGCCACTACACCTTTTCCATGCTGGTAACTGATTT 1225
Db 274 ValValValPheAlaValSerTrpLeuProLeuHisAlaPheGlnLeuAlaValAspIle 293
Qy 1226 RATGACAATCTTATTCAAAATAGGCATTTCAAGTTGGTGTATGTTGATTTGTCATTGTTG 1285
Db 294 AspSerGlnValLeuAspLeuLysGluTyrLysLeuIlePheThrValPheIleIle 313
Qy 1286 GCATGATGCTGTGTTGTTTAAATCAATCTATATGTTTCTTAAATGAGTAA 1345
Db 314 AlaMetCysSerThrPheAlaAsnProLeuLeuTyrGlyTrpMetAsnSerAsnTyrArg 333
Qy 1346 GCTGATTAGTGTCCCTTATACACTGT 1372
Db 334 LysAlaPheLeuSerAlaPheArgCys 342

RESULT 10
I52315
G protein-coupled receptor UHR-1 - rat
C:Species: Rattus sp. (rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C:Accession: I52315
R:Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.

Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A:Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from :
A:Reference number: I52315; MUID:95251659; PMID:773930
A:Accession: I52315
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-370 <RES>
A:Cross-references: GB:IS77867; NID:g998527; PIDN:AAB34129.1; PID:g998528
C:Superfamily: neurokinin 1 receptor

Alignment Scores:
Pred. No.: 5,33e-28 Length: 370
Score: 404.00 Matches: 111
Percent Similarity: 41.07% Conservative: 66
Best Local Similarity: 25.75% Mismatches: 138
Query Match: 16.29% Indels: 116
DB: 1 Gaps: 9

US-09-771-956-4 (1-1406) x I52315 (1-370)
Qy 86 GCCACAGAAATAACTCTCTCCACTCGGAATTTCTGATTTCCAGTCTGGGATGACTAT 145
Db 32 AlaserGluSerAsnValSerAlaThrValPProAlaAlaVal---ThrProPhe 50
Qy 146 AAAAGC-----AGCTAGATGACTTACAGTATTTTCTGATTTGGGCTCTATACATTTGTA 199
Db 51 GlnSerLeuGlnLeuValHisGlnLeuLysGlyLeuIleValMetLeuTyrSerIleVal 70
Qy 200 AGTCTTCTTGGTCTTATGGGAATCTACTATTTTAAATGGCTCTCATGAAAGCGTAAT 259
Db 71 ValValValGlyLeuValGlyAsnCysLeuLeuValLeuValIleAlaArgValArg 90
Qy 260 CAGAACTACGTAACCTTCTCATAGCAATCTGGCCTTTCTGATATCTGTTGTTG 319
Db 91 LeuHisAsnValThrAsnPheLeuIleGlyAsnLeuAlaLeuSerAspValLeuMetCys 110
Qy 320 CTGTTTGTCTCACTTTCACTTCACTGACGTCTGCTTCTGCTGGATCAG---TGGATGTTGGC 376
Db 111 AlaAlaCysValProLeuThrLeuAlaTyrAlaPheGluProArgGlyTrpValPheGly 130
Qy 377 AAAGTCATGTCATATTATGCTTTTCTCAATGTGTCTGATTTGTTGTTCAACTTTA 436
Db 131 GlyGlyLeuCysHisLeuValPhePheLeuGlnProValThrValTyrValSerValPhe 150
Qy 437 ATTTTAATCAATTCCTGTCAGTATCATATAAATCAATCAATCAATCAATCAAT 496
Db 151 ThrLeuThrThrIleAlaValAspArgTyrValValLeuValHisProLeuArgArg 170
Qy 497 TTAACAGCAAAACCATGGCTACTTCTGATAGTACTGTCTGGACACTAGTTTTCATC 556
Db 171 IleSerLeuLysLeuSerAlaTyrAlaValLeuGlyIleTrpAlaLeuSerAlaValLeu 190
Qy 557 TGTCTCCCTCCAGTGTTCACAGCTTGTGGAACTTCAAGAAACATTTGTTTCAGCA 616
Db 191 AlaLeuProAlaAlaValHisThrTyrHisValGluLeuLysPro----- 205
Qy 617 TTGCTGAGCAGCAGGATTTTATGTTGATGCTATGCGCATCT---GATTTCATACAGAA 673
Db 206 -----HisAspValArgLeuCysGluGluPheTrpGlySerGlnArgGlnArgGln 223
Qy 674 GCCTTACTATCTCTTTTATGCTAGTTCAGTATATTTCTGCCCTTAGTTGCTTACTGTA 733
Db 224 IleTyrAlaTrpGlyLeuLeuGlyThrTyrLeuLeuProLeuAlaIleLeuLeu 243
Qy 734 AGTCATACAGTGTCTGCAGAGTATAAGCTGTGGATTGTCCAAACAAAGAAACAGACTT 793
Db 244 SerTyrValArgVal----- 248
Qy 794 GAAGAAATGAGATGATCAACTTAACCTTTCATCCATCCAAAGAGTGGCGCTCAGGTG 853
Db 249 -----SerVal 250
Qy 854 AAACCTCTGCGAGCCATAATGGAGTTATTCATTATCAATCAAAACAAACAGAGATAT 913

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Db      251 LysLeu-----||||||-----ArgAsnArg--- 255
QY      914 AGCAAGACAGACGATGTGTACTCTGCTCCAGAAAGACCTTCTCAAGAGAACACCTCC 973
Db      256 -----ValValProGlySerValThrGlnSerGlnAlaAspTrpAsp 269
QY      974 AGAATACTTCCAGAAAACTTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTC 1033
Db      270 Arg-----|||----- 270
QY      1034 ATACCAGGGTCCCACTGTCTTTGAGATAAACCTGAAGAAATTCAGATGTTATGAA 1093
Db      270 ----- 270
QY      1094 TTGAGAGTAAACGTTCTCTTACAGATAAAAGAGATCTCGAAGTGTCTTCTACAGA 1153
Db      271 -----AlaArgArgArgArgThrPheCysLeu 279
QY      1154 CTGACCATCTGATATTAGTATTGCTGTAGTGGATGCCACATACACCTTTTCCATGTG 1213
Db      280 LeuValValValValValPheAlaLeuCysTrpLeuProLeuHisIlePheAsnLeu 299
QY      1214 GTAACGTATTAAAGACAACTTTATTCAATAGGCAATTTCAAGTGGTGTATTGCAAT 1273
Db      300 LeuArgAspLeuAspProArgAlaIleAspProTyrAlaPheGlyLeuValGlnLeu 319
QY      1274 TGTCAATTTGTTGGGATGATGTCCTGTGTTCTTAATCAATCTATATGAGTGGTGTCTTAAT 1333
Db      320 CysHisTrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHis 339
QY      1334 AATGGATTAAAGCTGATTAGTGTCCCTTATA 1366
Db      340 AspSerPheArgGluGluLeuArgLysMetLeu 350

RESULT 11
JC7809
sulfakinin receptor protein, DSK-R1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C:Accession: JC7809
R:Kubisiak, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.; Zantello, M.R.;
Biochem. Biophys. Res. Commun. 291, 313-320, 2002
A:Title: Cloning and functional expression of the first Drosophila melanogaster sulfakinin
A:Reference number: JC7809; PMID:11846406; M0ID:21835488
A:Accession: JC7809
A:Molecule type: mRNA
A:Residues: 1-584 <KUB>
C:Cross-references: UNIPROT:Q7M3J6; GB:AX128640
C:Comment: This receptor, the first functionally active orphan Drosophila sulfakinin G-P
actions
C:Genetics:
A:Map position: 17
F:115-139/Domain: transmembrane region #status predicted <TM1>
F:149-167/Domain: transmembrane region #status predicted <TM2>
F:189-207/Domain: transmembrane region #status predicted <TM3>
F:229-250/Domain: transmembrane region #status predicted <TM4>
F:275-300/Domain: transmembrane region #status predicted <TM5>
F:431-454/Domain: transmembrane region #status predicted <TM6>
F:467-491/Domain: transmembrane region #status predicted <TM7>

Alignment Scores:
Pred. No.: 3 35e-26 Length: 584
Score: 384.00 Matches: 119
Percent Similarity: 41.15% Conservative: 81
Best Local Similarity: 24.49% Mismatches: 186
Query Match: 15.48% Indels: 100
DB: 2 Gaps: 15

US-09-771-956-4 (1-1406) x JC7809 (1-584)
QY      35 CAGCACTATATATGAGTTTACAGCTCCAGCAGTATTATACAG-----ACACTT 85

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Db      69 ArgAspGlyTyrMetAspThrGluProSerAspLeuValThrGluLeuAlaPheSerLeu 88
QY      86 GCCACGAGAAATAT-----ACTGCTGCCACTCGGAATCTT 121
Db      89 GlyThrSerSerProSerProSerThrProAlaSerSerSerThrThrThr 108
QY      122 GATTTCCTCCAGTCTGACATATAAAGCAGGTAGTACCTTACAGTATTTCCTGATT 181
Db      109 GlyMetProValTrp-----LeuIle 115
QY      182 GGGCTCTATACATTTCTAAGTCTTTTGGCTTTATGGGAATCTACTTATTTAAATGGCT 241
Db      116 ProSerTyrSerMetIleLeuLeuPheAlaValLeuGlyAsnLeuValIleSerThr 135
QY      242 CTCATGAAAACGGTAAATCAGAAGACTAGGTAACTTCTCATAGGCACTGCGCTTT 301
Db      136 LeuValGlnAsnArgMetArgThrIleThrAsnValPheLeuLeuAsnLeuAlaIle 155
QY      302 TCTGATATCTTGTGTGCTGTTTGTCTCACCTTTTCCACTGACCTCTCTTGTGTGAT 361
Db      156 SerAspMetLeuLeuGlyValLeuCysMetProValThrLeuValGlyThrLeuLeuArg 175
QY      362 CAGTGGATGTTGGCAAGTCATGTCATATATATGCTTTTCTTCATGTGTGCTGATT 421
Db      176 AsnPheIlePheGlyLeuPheLeuCysLysLeuPheGlnPheSerGlnAlaAlaSerVal 195
QY      422 TTGGTTTCAACTTTAATTTAATATCAATTGCAATTTGTCAGGTATCATATGATAAACAAT 481
Db      196 AlaValSerSerTrpThrLeuValAlaIleSerCysGluArgTyrTyrAlaIleCysHis 215
QY      482 CCATATCTAATAAT-----TTAACAGCAAAACCATGGCTACTTCTTATGATGCTGCT 535
Db      216 ProLeuArgSerArgSerTrpGlnThrIleSerHisAlaTyrLysIleIleGlyPheIle 235
QY      536 TGGACACTAGGTTTGGCCATCTGTTCCCTCCAGTGTTCACAGTCTTCTGGAACCTT 595
Db      236 TrpLeuGlyGlyLeuLeuCysMetThrProIleAlaValPheSerGlnLeuIlePro--- 254
QY      596 CAAGAAACATTTGGTTACAGATTGTCAGCAGCAGC-----TATTATGTTGAG 646
Db      255 -----ThrSerArgProGlyTyrCysLysCysArgGlu 265
QY      647 TCATGCGCATCTGATTATCATACAGAAATGCTTTACTATCTCTTTATTGCTAGTACGAT 706
Db      266 PheTrpProAspGlnGlyTyrGluLeuPheTyrAsnIleLeuLeuArgThrLeuLeuVal 285
QY      707 ATTCTGCCCTTAGTTTGTCTTACTTAAAGTCATACAAGTGTCTGCAGAGATATAGCTGT 766
Db      286 ValLeuProLeuLeuValLeuCysValAlaTyrIleLeuIleThrArgThrLeuLeuVal 305
QY      767 GGATTGTCCCAACAAAGAAACAGAA-----CTTGAAGAAATGAGATGATCACTTACTCTT 823
Db      306 GlyMetAlaLysAspSerGlyArgIleLeuGlnGlnSerLeuProValSerAlaThrThr 325
QY      824 CATCCATCCAAAGAGTGGGCTCAGGTGAAACTCTCTGGCAGCCATAAATGGAGTTAT 883
Db      326 AlaGlyGlySerAlaProAsnProGlyThr----- 335
QY      884 TCATTATCAAAAAACACAGAAAGATATAGCAAGAGACAGCAGCATGTGTGTTA----- 937
Db      336 -----SerSerSerSerAsnCysIleLeuValLeu 345
QY      938 -----CCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGCAATACTTCCAGAA 988
Db      346 ThrAlaThrAlaValTyrAsnGlnAsnSerAsnAsnAsnGlyAsnSerGluGlySer 365
QY      989 AACTTTGGCTCTGTAAAGAGTCAGCTCTCTTCATCCAGTAAGTTCATACCGGGGTCCCC 1048
Db      366 AlaGlyGlyGlySerThrAsnMetAlaThrThrThrThrThrThrThrThrThrThr 385
QY      1049 ACTTGCTTTGAGATA-----AACCTGGAAGAAAT 1078

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Db 386 ThrValIleThrThrThrThrThrThrValThrLeuAlaLysThrSerSerProSer 405
 Qy 1079 TCAGATGTCATGAATGAGAGTAAAAAGTTCT-----GTTCAAGAATAAAA 1126
 Db 406 IleArgValHisAspAlaAlaLeuArgAsnGluAlaLysThrLeuGluSerLys 425
 Qy 1127 AAGAGATCTCGAAGTGTGTTTCTCAGACTGACCACTGATATAGTATTGCTGTAGT 1186
 Db 426 LysArg-----ValValLysMetLeuPheValLeuValLeuGluPhePheLeu 442
 Qy 1187 TGGATGCCACTACACCTTTTCCAT-----GTGGTAACTGAT 1222
 Db 443 TrpThrProLeuTyrrValIleAsnThrMetValMetLeuIleGlyProValValTyrrGlu 462
 Qy 1223 TTYAATGAC---AATCTATTTCAAATAGGCATTTCAGITGGTGATTGCAATTGTGCAT 1279
 Db 463 TyrValAspTyrrAlaIleSer-----PheLeuGln 473
 Qy 1280 TTGTTGGCGATGATGTCGTGTCTTAAATCCAATTCATATGGGTTCTTAAATAATGGG 1339
 Db 474 LeuLeuAlaTyrrSerSerSerCysAsnProIleThrTyrrCysPheMetAsnAlaSer 493
 Qy 1340 ATTAAAGCTGATTTAGTG 1357
 Db 494 PheArgArgAlaPheVal 499

RESULT 12
 JC5599
 cholecystokinin-A receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
 C:Accession: JC5599
 R:Lacourse, K.A.; Lay, J.M.; Swenberg, L.J.; Jenkins, C.; Samuelson, L.C.
 Biochem. Biophys. Res. Commun. 236, 630-635, 1997
 A:Title: Molecular structure of the mouse CCK-A receptor gene.
 A:Reference number: JC5599; MUID:97396148; PMID:9245702
 A:Accession: JC5599
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-436 <LAC>
 A:Cross-references: UNIPROT:Q08786
 A:Note: translation not complete
 C:Comment: This receptor belongs to the seven transmembrane G-protein coupled x
 cder contraction, and cholecystokinin inhibition of food intake.
 C:Superfamily: neurokinin 1 receptor
 F:42-67/Domain: transmembrane #status predicted <TM>

Alignment Scores:		
Pred. No.:	1.4e-25	Length: 436
Score:	377.00	Matches: 109
Percent Similarity:	44.06%	Conservative: 84
Best Local Similarity:	24.8%	Mismatches: 175
Query Match:	15.20%	Indels: 70
DB:	2	Gaps: 13

US-09-771-956-4 (1-1406) x JC5599 (1-436)

Qy 83 CTTGCCACAGAAATAACTGCTGCCACTCGGAATTCGTATTCCTCCAGTCGGATGAC 142
 Db 20 LeuGlyLeuGluAsnGluThrLeuPheCysLeuAspGlnProGlnProSer---LysGlu 38
 Qy 143 TATAAAGCAGGTGATGACTTACAGTATTTCTGATTTGGCTCTATACATTTGTAAGT 202
 Db 39 TrpGlnSerAlaValGlnIleLeu-----LeuTyrrSerPheIlePhe 52
 Qy 203 CTTCTTGCTTTATGGGAATCTACTTATTATTAATGGCTCTCATGAAAAGCGTAAATCAG 262
 Db 53 LeuLeuSerValLeuGlyAsnThrLeuValIleThrValLeuIleArgAsnLysArgMet 72
 Qy 263 AAGACTACGGTAAACTTCCTCATAGCAATCTGGCTTTTCTGATATCTTGTTGTGCTG 322
 Db 73 ArgTrpValThrAsnIlePheLeuLeuSerLeuAlaValSerAspLeuMetLeuCysLeu 92

	QY	323	TTTTTGCTACCTTTTACACTGAGCGTGTCTGCTGGATCAGTCGGATGTTTGCACAAGTC	382
	DQ	93	PheCysMetProPheAsnLeuLeuLeuProAsnLeuLeuLeuAaspHeIlePheGlySerAla	112
	QY	383	ATGTGCCATATTATGCGCTTTTCTTCAATGTGTCTCAGTTTGGTTTCAAATTTTAATTTA	442
	DQ	113	ValCysLysThrThrThrTyrrPheMetGlyThrSerValSerValSerThrPheAsnLeu	132
	QY	443	ATAATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAATTTA--	499
	DQ	133	ValAlaIleSerLeuGluArgGlyrGlyAlaIleCysArgProLeuGlnSerArgValTrp	152
	QY	500	--ACAGCAAACCATCGCTACTTTTCTGATAGCTACTGTCTGGACACTAGGTTTGGCAATC	556
	DQ	153	GlnThrLysSerHisAlaLeuLysValIleAlaAlaThrTrpCysLeuSerPheThrIle	172
	QY	557	TGTTCTCCCCTCCAGNGTTTCCACAGTCTGTGGAACTTCAAGAAAAATTTGTTGTCAGCA	616
	DQ	173	MetThrProTyrrProIleLeuTyrrSerAsnLeuValProPheThrLysAsnAsnGlnThr	192
	QY	617	TTGCTGAGCAGCAGGTATTATGATTGTGTGAGTCATGCGCATCTGATTCATACAGAATTGCC	676
	DQ	193	AlaAsnMetCysArgPheLeuLeu-----ProSerAspAlaMetGlnGlnSer	208
	QY	677	TTTACTATCTTTATTGCTAGTTCAGTATATTCTGCTTACTTGTCTTACTGTAAGT	736
	DQ	209	TrpGlnThrPheLeuLeuLeuIleLeuPheLeuIleProGlyValValMetValValAla	228
	QY	737	CATACRAGTGTCTGCAGAAAGTATPAAGCTGTGGATTGTCCAACAAAAGAAACAGACTTGAA	796
	DQ	229	TyrGlyLeuIleSerLeuGluLeuLeuTyrrGlnGlyIleLysPheAspAlaSerGln----	246
	QY	797	GAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAAGAGTGGCGCTCAGGTGAAG	856
	DQ	247	-----LysLysSerAlaLysGluLysArg	254
	QY	857	CTCTCT-----GGCAGCCATAAATGAGTATTATCATTCATCAAAAACACAGAAGA	907
	DQ	255	LeuSerSerGlyGlyGlyGlyGlyGlySerSerSer-----Ser	268
	QY	908	AGATATAGCAAGAAGACGACATGTGTGTACCTGCTCCAGAAAAGACCTTCTCAAGAGAAC	967
	DQ	269	ArgTyrrGluAspSerAspGlyCystrYrrLeuGlnLysSerArgProProArgLysLeuGlu	288
	QY	968	CACTCCAGAATCTTCCAGAAAACTTTGGCTCTGTGAAGAGTCAGCTCTCTTCCATCCAGT	1027
	DQ	289	-----LeuGlnGlnLeuSerThrSerSer	296
	QY	1028	AAGTTCATACCAGGGTCCCCACTTGTCTTTGAGATAAACCTGAAGAAAAATTCAGATGTT	1087
	DQ	297	-----SerGlyGlyArgIle	301
	QY	1088	CATGAATTGAGAGTAAACCGTTCTGTTCACGAATAAAAAAGAGATCTCGAAGTGTTTTC	1147
	DQ	302	AsnArgIleArgSerSerGlySerAlaAlaAsnLeuIleAlaLysArg---ValIle	320
	QY	1148	TACAGACTGACCATCTGATATAGTAGTATTGCTGTAGTTAGTGATGCCACTACACCTTTTC	1207
	DQ	321	ArgMetLeuIleValIleValIlePhePheLeuCysTrpMetProIlePheSerAla	340
	QY	1208	CATGTGGTAACTGATTTTAATGACAATCTTTATTTCAAATAGGCAATTTCAAG-----	1258
	DQ	341	AsnAlatrArpAlaTyrr--AspThrValSerAlaGluLysHisLeuSerGlyThrPro	359
	QY	1259	TTGTTGATGTCATTCTTCATTTCTGGCGATGATGCTGTTGCTTCTTAATCCAAATCTTA	1318
	DQ	360	IleSerPheIleLeu-----LeuLeuSerTyrrThrSerSerCysValasnProIleIle	377
	QY	1319	TATGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGTGCCCTTTATFACACTGT	1372
	DQ	378	TyrrCysPheMetAsnLysArgPheArgLeuGlyPheMetAlatrPheProCys	395

RESULT 13

S50150
gastric CCK-A receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
C:Accession: S50150
R:Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
Biochim. Biophys. Acta 1219, 321-327, 1994
A:Title: Cloning and expression of the rabbit gastric CCK-A receptor.
A:Reference number: S50150; MUID:95002144; PMID:7918628
A:Accession: S50150
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-427 <REU>
C:Superfamily: neurokinin 1 receptor

Alignment Scores:
Pred. No.: 2,11e-25 Length: 427
Score: 375.00 Matches: 104
Percent Similarity: 43.81% Conservative: 73
Best local Similarity: 25.74% Mismatches: 155
Query Match: 15.12% Indels: 72
DB: 2 Gaps: 9

US-09-771-956-4 (1-1406) x S50150 (1-427)

QY	185	CTCTATACATTGTAAGTCTTCTGGCTTTATGGGATCTACTATTATTAATGGCTCTC	244
Db	47	LeuTyrSerLeuIlePheLeuLeuSerValLeuGlyAsnThrLeuValIleThrValLeu	66
QY	245	ATGAAAGCGTAAATCAGAACATACGGTAAACTTCTCATAGCAATCTGGCCCTTTCT	304
Db	67	IleArgAsnLysArgMetArgThrValThrAsnIlePheLeuLeuSerLeuAlaIleSer	86
QY	305	GATATCTGGTGTGCTGTTTGTCTACCTTTCACATGACGTCTGCTGCGATCAG	364
Db	87	AspLeuMetLeuLysLeuPheCysMetProPheAsnLeuIleProAsnLeuLeuLysAsp	106
QY	365	TGGATGTTTGGCAAGTCATGTCATATTCCTTCTCAATGTCGTGCTGCTTTC	424
Db	107	PheIlePheGlySerAlaLeuLysLysThrThrThrLysLeuMetGlyThrSerValSer	126
QY	425	GTTTCAACTTTAATTAATCAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG	484
Db	127	ValSerThrLeuAsnLeuValAlaIleSerLeuGluArgTyrGlyAlaIleCysLysPro	146
QY	485	ATATCTAATAATTTA-----ACAGCAACCATGGCTACTTCTGTAGTACTGCTGG	538
Db	147	LeuGlnSerArgValTrpGlnThrLysSerHisAlaLeuLysValIleAlaAlaThrTrp	166
QY	539	ACACTAGTGTTCGCATCTGTTCTCCCTTCACAGTGTTCACAGTCTGTGGAACTTCAA	598
Db	167	CysLeuSerPheAlaIleMetThrProTyrProIleTyrSerAsnLeuValProPheThr	186
QY	599	GAACATTTGTTGAGCATCTGCTGAGCAGCAGGATTTATTGTTGAGTTCATGGCATCT	658
Db	187	LysThrAsnAsnGlnThrAlaAsnMetCysArgPheLeuLeu-----ProSer	202
QY	659	GATTTCATACAAATGTCCTTACTATCTCTTATTGCTAGTTCAGTATATTCGCGCTTA	718
Db	203	AspValMetGlnGlnAlaTrpHisThrPheLeuLeuLeuIleLeuPheLeuIleProGly	222
QY	719	GTTTGTCTTACTGTAAGTCATACAAAGTGTCTGCGAAGTATAGCTGTGGAATGTCAC	778
Db	223	IleValMetMetValAlaIle-----	229
QY	779	AAAGAAACACAGACTTGAAGAAATGACATGATCAACTTAATCTTCATCCATCCAAAAAG	838
Db	230	-----GlyMetIleSerLeuGluLeuLeuGlnGly-----	239
QY	839	AGTGGGCTCAGGTGAACCTCTCTGGCGCAGCAATAATGGAGTTATTCATTCACAAAAA	898
Db	240	-----IleLysPheAspAlaSerGlnLysLysSer-----AlaLys	251

QY	899	CACAGAAGA-----AGATATAGCAAGACAGACATGCTGTGTTACT	940
Db	252	GlutArgLysAlaSerThrGlySerGlyArgPheGluAspAsnAspGlyCysTyrLeuGln	271
QY	941	GCTCCAGAAGACCTTCTCAAGAACCACTCCAGAATACCTCCAGAAAACTTTGGCTCT	1000
Db	272	Arg---SerLysProThrArgGlnLeuGluLeuGlnLeuSerGlyGlyGlyGly	290
QY	1001	GTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTTCATACCAGGGTCCCACTTGTCTTGAG	1060
Db	291	ArgValSerArgIleHisSerSer-----	298
QY	1061	ATAAACCTCGAAGAAATTCAGATGTTTCAGTAATGAGAGTAAACGTTCTGTTACAGA	1120
Db	299	-----SerSerAlaAlaLeuMetAlaLysLysArgValIleArg	312
QY	1121	ATAAAAAAGAGATCTCGAAGTGTTCCTACAGACTGACCATATGATATTGCT	1180
Db	313	Met-----LeuMetValIleValLeuPhePhe	322
QY	1181	GTTAGTGGATCCCACTACACCTTTTCCATGCGTAAGTATTTAAATGACAAATCTTATT	1240
Db	323	LeuCysTrpMetProIlePheSerAlaAsnAlaTrpArgAlaTyrAspThrValSerAla	342
QY	1241	TCAATAGGCATTTCAAGTGTGTTGCTGATTCATTTGCTGTTGGGCGATGTCCTGT	1300
Db	343	GluArgArgLeuSerGlyThrProIleSerPheIleLeuLeuLeuSerTyrThrSerSer	362
QY	1301	TGCTTAATCCAAATCTATATGTTTCTTAATATGGGATTAAGCTGATTAGTGTCC	1360
Db	363	CysValAsnProIleIleTyrCysPheMetAsnLysArgPheArgLeuGlyPheMetAla	382
QY	1361	CTTATACACTGT	1372
Db	383	ThrPheProCys	386

RESULT 14
A42685
cholecystokinin receptor type A - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42685; J04225; PC2213
R:Wank, S.A.; Harkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slatery, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 3125-3129, 1992
A:Title: Purification, molecular cloning, and functional expression of the cholecystokinin
A:Reference number: A42685; MUID:92212981; PMID:1313582
A:Accession: A42685
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-444 <WAN>
A:Experimental source: pancreas
A:Notes: sequence extracted from NCBI backbone (NCBI:93814, NCBI:93815)
R:Takata, I.; Takiguchi, S.; Funakoshi, A.; Kono, A.
Biochem. Biophys. Res. Commun. 213, 958-966, 1995
A:Title: Gene structure of rat cholecystokinin type-A receptor.
A:Reference number: J04225; MUID:95382845; PMID:7654260
A:Accession: J04225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <TAK>
A:Cross-references: DBJ:050608; NID:gl100752
R:Mantamadiotis, T.; Baldwin, G.S.
Biochem. Biophys. Res. Commun. 201, 1382-1389, 1994
A:Title: The seventh transmembrane domain of gastrin/CCK receptors contributes to non-pep
A:Reference number: PC2213; MUID:94296413; PMID:8024583
A:Accession: PC2213
A:Status: preliminary
A:Molecule type: protein
C:Comment: This G-protein-coupled receptor is present in the gastrointestinal system, vas
, smooth muscle contraction of the gallbladder and stomach. It is capable of activating i
during the subsequent release of intracellular calcium.

Db 262 -----LysLysSerAlaLysGluLysLys 269

QY 857 CTCTCT--GGCAGCCATAAATCGAGTTATTTCATTCATCAAAAAACACACAGAAGAGATAT 913

Db 270 ProSerThr.GlySer-----SerThrArgTyr 278

QY 914 AGCAAGAAGACAGCATGTGTGTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACCTCC 973

Db 279 GluAspSerAspGlyCysTyrLeuGlnLysSerArgProProArgProGluLeuGln 298

QY 974 AGAATACCTCCAGAAAACCTTGGCTCTGTAAGAAGTCAGCTCTCTTCATCCAGTAAGTTC 1033

Db 299 GlnLeuSerSerGlySerGlyGlySerArgLeuAsnArgIleArgSerSer----- 315

QY 1034 ATACCAGGGGTCCCACTTGCTTTGGAGATAAAACCTCAAGAAAATTCAGATGTTTCATGAA 1093

Db 316 -----SerSerAlaAlaAsn 320

QY 1094 TTGAGAGTAAACGTTCTGTTACAGAATAAAAAAGAGATCTCGAAGTGTTTCTACAGA 1153

Db 321 LeuIleAlaLysLysArgValIleArgMet----- 330

QY 1154 CTGACCATCTGATATTAGTATTGCTGTGTTAGTTGGATGCGCACTACACCTTTTCCATGTG 1213

Db 331 LeuIleValIleValValLeuPheLeuCysTyrMetProIlePheSerAlaAsnAla 350

QY 1214 GTAACCTGATTTAATGACAACTTATTTCAAATAGGCATTTTCAAG-----TTGGTG 1264

Db 351 TrpArgAlaTyr--AspThrValSerAlaGluLysHisLeuSerGlyThrProIleSer 369

QY 1265 TATTGCATTTGTCATTTGTTGGCATGATCTCTGTTGTCTTAATCAAATCTATATATGGG 1324

Db 370 PheIleLeu-----LeuLeuSerTyrThrSerSerCysValAsnProIleIleTyrCys 387

QY 1325 TTTCCTTAATATGGGATTAAAGCTGATTTTAGTGTCCCTTATACACTGT 1372

Db 388 PheMetAsnLysArgPheArgLeuGlyPheMetAlaThrPheProCys 403

RESULT 15

A41738

N;Alternate names: fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: A41738

J;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-13, 1992

A;Title: Cloning, functional expression, and developmental regulation of a neuro-

A;Reference number: A41738; MUID: 92112730; PMID: 1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIR>

A;Cross-references: UNIPROT:P25931; GB:M01490; NID:G157996; PIDN:AAA28727.1; PT:

C;Genetics:

A;Gene: FlyBase:Nepyr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Alignment Scores:

Pred. No.:	1,1e-24	Length:	449
Score:	367.00	Matches:	99
Percent Similarity:	38.02%	Conservative:	66
Best Local Similarity:	22.81%	Mismatches:	123
Query Match:	14.80%	Indels:	146
DB:	2	Gaps:	12

US-09-771-956-4 (1-1406) x A41738 (1-449)

QY 137 GATGACTATAAAACGAGTGTAGATGACTTA-----CAGTATTTTCTGATT----- 181

Db 74 AspAspTyrAspLeuLeuSerGluAspMetTrpSerSerAlaTyrPheLysIleVal 93

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QY 182 ---GGGCTCTATACATTGTGAAGTCTTCTGGCTTTATGGGAATCTACTTAITTTAATG 238
Db 94 TyrMetLeuTyrIleProIlePheIlePheAlaLeuIleGlyAsnGlyThrValCysTyr 113
QY 239 GCTCTCATGAAGAAGCGTAATCAGAGACTACGGTAACCTTCCTCATAGGAATCTGGCC 298
Db 114 IleValTyrSerThrProArgMetArgThrValThrAsnTyrPheIleAlaSerLeuAla 133
QY 299 TTTTCTGATATCTTGGTGTGCTGTTTGGCTCACCTTTCACACTGACGCTGTGC---TTG 355
Db 134 IleGlyAspIleLeuMetSerPhePheCysGluProSerSerPheIleSerLeuPheIle 153
QY 356 CTGATCAGTGGATGTTTGGCAAGTCAATGCGCATATATGCGCTTTCCTCAATGRTG 415
Db 154 LeuAsnTyrTrpProPheGlyLeuAlaLeuCysHisPheValAsnTyrSerGlnAlaVal 173
QY 416 TCAGTTTGGTTTCAACTTTAATTTAATATCAATGCCATTGCCATTGTCAGGTATCATATGATA 475
Db 174 SerValLeuValSerAlaTyrThrLeuValAlaIleSerIleAspArgTyrIleAlaIle 193
QY 476 AAACATCCCATATCTAATAATTAAACAGCAACCATGGCTACTTCTGTAGTACTGTCTC 535
Db 194 MetTrpProLeuLysProArgIleThrLysArgTyrAlaThrPheIleIleAlaGlyVal 213
QY 536 TGGACACTAGGTTTGGCATCTGTCTCCCTCCAGTG----- 574
Db 214 TrpPheIleAlaLeuAlaThrAlaLeuProIlePheValSerGlyLeuAspIlePro 233
QY 575 -----TTTCACAGCTCTTGTGGAACTTCAAGAAACATTTGGTTCAGCATTCCTGAGC 625
Db 234 MetSerProTrpHisThrLysCysGlu----- 242
QY 626 AGCAGGTATTTATGTTGAGTCAATGCGCATCTGATTCATCAGAAATGCGTTTACTATC 685
Db 243 ---LystyrIleCysArgGluMetTrpProSerArgSerGlnGluTyrTyrThrLeu 261
QY 686 TCTTTATTTGCTAGTATATCTGCCCTTACTTGTCTTACTGTAAGTCAATACAAAGT 745
Db 262 SerLeuPheAlaLeuGlnPheValProLeuGlyValLeuIlePheThrTyrAlaArg 281
QY 746 GTCTGCAGAGATTAAGCTGTGAGTGTTCACAAAGAAACAGACTTGAAGAAATGAG 805
Db 282 IleThrIleArgVal----- 286
QY 806 ATGATCAACTTAACCTCTTCATCCATCCAAAGAGTGGGCTCAGGTGAACCTCTCTGGC 865
Db 286 ----- 286
QY 866 AGCCATAAATGGAGTTATTTCATTTCATCAAAAAACACAGAGAAGATATAGCAAGAAGACA 925
Db 287 -----TrpAla----- 288
QY 926 GCATGTGTGTTACCTGCTCCAGAAAGACCTTCTCAGAGAAACCACTCCAGAAATACTTCCA 985
Db 289 -----LysArgPro----- 291
QY 986 GAAAACTTTGGCTCTGTAAGAAGTCAAGTCTCTTCATCCAGTAAGTTCATACCAGGGGTC 1045
Db 292 -----ProGly--- 293
QY 1046 CCCACTGCTTTGAGATAAACCCTGAAGAAATTCAGATCTTCATGAATTCAGAGTAAAA 1105
Db 294 -----GluAlaGluThrAsnArgAspGlnArgMetAlaArgSerLys 307
QY 1106 CGTTCTGTACAGAAATAAAGAGATCTCGAAGTGTCTTCTACAGACTGACCATACTG 1165
Db 308 ArgLysMetValLysMet-----MetLeuThrVal 317
QY 1166 ATATTAGTATTGCTGTAGTGGATCCCACTACACCTTTTCCATGTGGTAACTGATTTT 1225
Db 318 ValIleValPheThrCysCysTrpLeuProPheAsnIleLeuGlnLeu----- 333
QY 1226 AATGACAACTTATTTCAAATAGCATTTTC-----AAGTTGGTGAT 1267
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Db 334 -----LeuLeuAsnAspGluGluPheAlaHisTrpAspProLeuProTyrValTrp 350
QY 1268 TGCATTTGTCATTTGTTGGCATGATGCTGTTCTTAAATCCAATTCATATGGGTTT 1327
Db 351 PheAlaPheHisTrpLeuAlaMetSerHisCysCysTyrAsnProIleIleTyrCysTyr 370
QY 1328 CTTAATAATGGGATTAAAGCTGATTAGTTAGTGTCCCTTATACAC 1369
Db 371 MetAsnAlaArgPheArgSerGlyPheValGlnLeuMetHis 384
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Search completed: October 21, 2004, 11:59:47
Job time : 76 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 21, 2004, 11:30:23 ; Search time 293.5 Seconds

(without alignments)
5512.618 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480
Sequence: 1 tttgtgtgtgcaaatgt.....attctcactgtttaccaagg 1406

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p_model -DEV=xlp
-Q=/cgn2/1/USPTO_spool_p/US09771956/runat_21102004_103737_9374/app_query.fasta.1.1543
-DB=UniProt_02 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRP=US09771956 @CGN 1.1 283 @runat_21102004_103737_9374 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NSG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	2385	96.2	455	1 NY5R HUMAN	Q15761 homo sapien
2	2330	94.0	445	2 AAH42416	AAH42416 homo sapi
3	2318	93.5	445	2 Q9K73	Q9K73 macaca mula
4	2241	90.4	446	2 Q25F1	Q25F1 cavia porce
5	2227	89.8	446	1 NY5R CANFA	Q82729 canis fami
6	2084.5	84.1	456	1 NY5R RAT	Q63634 rattus norv
7	2070	83.5	466	1 NY5R MOUSE	Q70342 mus musculu
8	2070	83.5	466	2 BAC32426	BAC32426 mus muscu
9	2028	81.8	446	1 NY5R PIG	Q97969 sus scrofa
10	1629.5	65.7	443	2 Q8QF2	Q8QF2 gallus galli
11	558	22.5	377	2 Q3733	Q3733 brachydanio
12	527	21.2	348	2 Q9Y6A4	Q9Y6A4 squalus aca
13	527	21.2	348	2 AAO62565	AAO62565 squalus aca
14	522.5	21.1	373	2 Q9Y6A5	Q9Y6A5 squalus aca
15	522.5	21.1	373	2 AAO62564	AAO62564 squalus a
16	502.5	20.3	377	2 Q9QGM3	Q9QGM3 gallus galli

17	497	20.0	371	1 NY6R RABIT	P78217 cryctolagus
18	487.5	19.7	382	1 NY1R CANFA	Q02813 canis fami
19	487.5	19.7	383	1 NY1R PIG	Q02835 sus scrofa
20	484.5	19.5	385	2 Q8QFM1	Q8QFM1 gallus galli
21	481.5	19.4	366	1 NY1R XENLA	P34992 xenopus lae
22	481.5	19.4	383	2 Q9K75	Q9K75 macaca mula
23	481.5	19.4	384	1 NY1R HUMAN	P25929 homo sapien
24	481.5	19.4	384	2 AA55647	AA55647 homo sapi
25	481.5	19.4	384	2 AAH71720	AAH71720 homo sapi
26	481	19.4	383	1 NY1R CAVPO	Q04573 mus musculu
27	480	19.4	382	1 NY1R MOUSE	P21555 rattus norv
28	480	19.4	382	2 AAH51420	AAH51420 mus muscu
29	480	19.4	382	2 NY6R MOUSE	O61212 mus musculu
30	476	19.2	371	1 NY6R MOUSE	BAC26875 mus muscu
31	476	19.2	371	2 BAC26875	Q9DNE6 gallus galli
32	473.5	19.1	385	1 NY2R CHICK	Q9YHXL gadus morhu
33	471.5	19.0	374	2 Q9YHX1	O97505 sus scrofa
34	466	18.8	375	2 Q6YH0	Q6YH0 macaca mula
35	466	18.8	375	2 AAH28939	AAH28939 macaca mu
36	464.5	18.7	375	1 NY4R HUMAN	P50391 homo sapien
37	464.5	18.7	375	2 Q6FH06	Q6FH06 homo sapien
38	464.5	18.7	375	1 NY4R RAT	Q63447 rattus norv
39	464	18.7	375	2 O57463	O57463 brachydanio
40	459	18.5	371	2 Q6Y6A6	Q6Y6A6 squalus aca
41	459	18.5	371	2 AAO62563	AAO62563 squalus a
42	459	18.5	381	2 Q8BW1	Q8BW1 mus musculu
43	458.5	18.5	385	1 NY2R MOUSE	P97295 mus musculu
44	458.5	18.5	385	1 NY4R MOUSE	Q61041 mus musculu
45	458	18.5	375	1 NY4R MOUSE	

ALIGNMENTS

RESULT 1

NY5R_HUMAN STANDARD; PRT; 455 AA.
ID Q15761; Q92916;
AC NY5R_HUMAN
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neuropeptide Y receptor type 5 (NPY-5 receptor) (Y5 receptor) (NPY5).
DE receptor) (NPY5).
GN Names=NPY5R; Synonyms=NPYR5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCSI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Hippocampus;
RC MEDLINE=96317589; PubMed=8700207;
RA Gerald C., Walker M.W., Criscione L., Gustafson E.L.,
RA Batzl-Hartmann C., Smith K.E., Vayssie P., Durkin M.M., Laz T.M.,
RA Lineneyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,
RA Taber R.I., Branchek T.A., Weinschank R.L.;
RT 'A receptor subtype involved in neuropeptide-Y-induced food intake.';
RL Nature 382:168-171(1996).
[2]
RN SEQUENCE OF 11-455 FROM N.A.
RP MEDLINE=96421636; PubMed=8824284;
RX Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,
RA Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,
RA Sadowski Y., Schaefer J., Velazquez N., McCalles M.L.;
RT 'Identification of a novel hypothalamic neuropeptide Y receptor associated with feeding behavior.';
RL J. Biol. Chem. 271:26315-26319(1996).
[3]
RN SEQUENCE OF 11-455 FROM N.A.
RP MEDLINE=97312686; PubMed=9169127;
RX Herzog H., Darby K., Ball H., Hori Y., Beck-Sickinger A., Shine J.;
RT 'Overlapping gene structure of the human neuropeptide Y receptor subtypes Y1 and Y5 suggests coordinate transcriptional regulation.';
RL Genomics 41:315-319(1997).

[4]
 RN SEQUENCE OF 11-455 FROM N.A.
 RA Kozatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RL sequenced by the Gichrie cDNA resource center (www.cdna.org).";
 CC Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity
 CC of this receptor is mediated by G proteins that inhibit adenylylate
 CC cyclase activity. Seems to be associated with food intake. Could
 CC be involved in feeding disorders.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain; hypothalamus.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Highest to tachykinins receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U56079; AAC50623.1; -;
 CC EMBL; U66275; AAC50741.1; -;
 CC EMBL; AY4320; AAC51295.1; -;
 CC EMBL; AY322538; AAB84351.1; -;
 CC Genbank; HGNC:7958; NPY5R.
 CC MIM; 602001; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004983; F: neuropeptide Y receptor activity; TAS.
 CC GO; GO:0007185; F: G-protein coupled receptor protein signalin. . . ; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC InterPro; IPR000393; NPY5R_receptor.
 CC InterPro; IPR000611; NPY_receptor.
 CC Pfam; PF00001; 7tm1; 1;
 CC PRINTS; PR00237; GPCR_HODOPSIN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
 CC PROSITE; PS0262; G_PROTEIN_RECP_F2_1;
 CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Phosphorylation; Transmembrane.
 FT DOMAIN 1 50 Extracellular (Potential).
 FT TRANSMEM 51 72 1 (Potential).
 FT DOMAIN 73 84 Cytoplasmic (Potential).
 FT TRANSMEM 85 105 2 (Potential).
 FT DOMAIN 106 125 Extracellular (Potential).
 FT TRANSMEM 126 147 3 (Potential).
 FT DOMAIN 148 167 Cytoplasmic (Potential).
 FT TRANSMEM 168 188 4 (Potential).
 FT DOMAIN 189 220 Extracellular (Potential).
 FT TRANSMEM 221 242 5 (Potential).
 FT DOMAIN 243 378 Cytoplasmic (Potential).
 FT TRANSMEM 379 401 6 (Potential).
 FT DOMAIN 402 414 Extracellular (Potential).
 FT TRANSMEM 415 438 7 (Potential).
 FT DOMAIN 439 455 Cytoplasmic (Potential).
 FT CARBOHYD 20 20 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 27 27 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 124 208 By similarity.
 FT LIPID 452 452 S-palmitoyl cysteine (Potential).
 SQ SEQUENCE 455 AA; 51990 MW; 95f2f475E5FBFF7 CRC64;
 Alignment Scores:
 Pred. No.: 2,696-188 Length: 455
 Score: 2385.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 1 Gaps: 0
 US-09-771-956-4 (1-1406) x NY5R_HUMAN (1-455)
 17 ATGCTCTTTTATCCAGCAGGACTATAATATGATTAGATTAGAGTCGACGAGTATTATAAC 76

Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
 QY 77 AAGACACTTGGCCACAGAGAAATAACTGCTGCACCTCGGAATTCCTGATTTCCAGTCTGG 136
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
 QY 137 GATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTCTGATTTGGGCTCTATACATTT 196
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
 QY 197 GTAAGTCCTCTGGCTTTATGATGGGAATCTACTATTATTAATGGCTCTCATCAAAAAGCGT 256
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
 QY 257 AATCAGAACACTACCGTAAACTTCCTCATAGCAATCTGGCCTTTCTGATATCTGGTT 316
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
 QY 317 GTGCTGTTTGTCTACCTTTACACTGACGCTGTCTTCTGGATCAGTGGATGTTGCG 376
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
 QY 377 AAAGTCATGTGCCATATTATGCTTTCTTCAATGTGTCTGAGTTTGGTTTCAACTTTA 436
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 QY 437 ATTTAAATATCAATTCGCATGTCAGGTATCATATGATAAAACATCCCATATCAATAAT 496
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
 QY 497 TTAACAGCAAAACATGGCTTACTTTCTGATAGTACTGTCTGGACACTAGGTTTGGCCATC 556
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
 QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTTCAGCA 616
 Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
 QY 617 TTGCTGACGACGAGGTATTATGCTGTGAGTCATGCGCATCTGATTATACAGAAATGCC 676
 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
 QY 677 TTTACTATCTCTTTATGCTAGTTCAGTATATCTGCCCTTAGTTTGTCTTACTGTAAAGT 736
 Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
 QY 737 CATACAGTGTCTGAGAAGTATAAGCTGTGGATTGTCCAAAGAAACAGACTTGAA 796
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 QY 797 GAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAAAGAGTGGGCCTCAGGTGAAA 856
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
 QY 857 CTCTCTGGCAGCCATAAATGGAGTATTATCATTCATCAAAAACAGACAGAGATATAGC 916
 Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
 QY 917 AAGAAGACAGCATGTGTGTACTCTCCAGAAAGACCTTCTCAAGAAACACACTCCAGA 976
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
 QY 977 ATACTTCCAGAAAACTTTGGCTCTCTAAGAGTCAAGTCACTCTTTCATCCAGTAAGTTCTA 1036
 Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
 QY 1037 CCAGGGGTCCCCACTTGTCTTGAGATAAAACCTGAGAAAAATTCAGATGTTTCATGAATTG 1096
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360
 QY 1097 AGAGTAAAAAGCTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTCTTCTACAGCTG 1156

Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 360
 QY 1157 ACCATCTAGTATTAGTATTTGCTGTTAGTTGGATGCCACTACACCTTTTCCATGTGCTA 1216
 Db 381 ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
 QY 1217 ACTGATTTAATGCAATCTTATTATTCAAATAGGCAATTCAGTTGGTGTATTCATTTGT 1276
 Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
 QY 1277 CATTTGTTGGCAGTATGCTGCTGTTGCTTAAATCCAAATTCATATGCTTCTTAATAAT 1336
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
 QY 1337 GCGATTAAAGCTGATTAGTGTCCCTTATACATGCTGCTTCATATG 1381
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455
 RESULT 2
 AAH42416 PRELIMINARY; PRT; 445 AA.
 ID AAH42416
 AC AAH42416;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Neuropeptide Y receptor Y5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the ENBL/GenBank/DBJ databases.
 DR EMBL; BC042416; AAH42416.1; -;
 SQ NEUROPEPTIDE; Receptor.
 SQ SEQUENCE 445 AA; 50726 MW; A2B0F3169DBA66BE CRC64;

Alignment Scores:
 Pred No.: 9,36e-184 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) X AAH42416 (1-445)

QY 47 ATGATTTAGAGTCGACGAGTATTATAACAAGACACTTGCACAGAGAAATAATACTGCT 106
 Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
 QY 107 GCCACTCGGAATCTGATTTCCAGTCTGGGATGACTATAAAGCAGCTGACGACTTA 166
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
 QY 167 CAGTATTTTCTGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 QY 227 CTTATTTTAAATGGCTCTCATGAAAAAGCTAATCAGAGACTACGGTAAACTTCCTCAT 286
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80
 QY 287 GGCATCTCGCCCTTTTCTGATATCTTGGTGTGGTGTCTTGTCTACCTTTCACACTGAGC 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGCTTCTGATCAGTGGATGTTTGGCAAGTCATGTGCATATATTATGCTTTTCTT 406
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
 QY 407 CAATGTGCTCAGTTTGGTTTCAACTTTTAAATATCAATTGCCATTGTCAGGTAT 466
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
 QY 467 CATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACCATGGCTACTTTCTGATA 526
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
 QY 527 GCTACTGTCTGGACACTAGTGTTCGCCATCTCTTCCCTTCCAGTGTTCACAGTCTT 586
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
 QY 587 GTGGAACCTTCAAGAAACATTTGTTTCCAGTATTCGTCAGCAGCAGGTATTATTGTGTGAG 646
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
 QY 647 TATGGCCATCTGATTCATACAGAAATGGCTTACTATCTCTTATCTTATGCTAGTTCAGTAT 706
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
 QY 707 ATTCTCCCTTGTGTTGCTTACTGTAACTCATACAAGTGTCTGCAGAAAGTATAAGCTGT 766
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
 QY 767 GGATTTCTCAACAAAGAAACACAGACTTGAAGAAAATGAGATGATCAACTTAATCTTCTAT 826
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAACCTCTGCGCAGCCATAAATGGAGTATTATCA 886
 Db 261 ProSerLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
 QY 887 TTTATCAAAAAACACAGAAAGAGATATATACAGAGACAGACAGCATGTGTGTACTGCTCA 946
 Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
 QY 947 GAAAGACCTTCTCAGAGAAACCACTCCAGAAATCTTCGAGAAACTTTGGCTCTGTAAAG 1006
 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
 QY 1007 AGTCAGCTCTCTTCTATCCAGTAAGTTTCACAGGGGTCCCACTTGTCTTTCAGATAAAA 1066
 Db 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
 QY 1067 CTTGAAGAAATTCAGATCTTCATGAATTTGAGAGTAAACCGTTCTCTTTCAGAGATAAAA 1126
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
 QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATATGATATTATTTCTGTGTAGT 1186

Db	361	LysArgSerArgSerValPheTyrArgLeuThrLeuLeuLeuValPheAlaValSer	380
QY	1187	TGGATGCCACTACACCTTTCCATGCTGGTAACACTGATTTTAATGACAATCTTATTTCAAAT	1246
Db	381	TrpMetProLeuHisLeuPheHisValThrAspPheAsnAspAsnLeuLeuSerAsn	400
QY	1247	AGGCAATTCAGTGGCTGATATGCAATTTGTCATTTGGCGCATGATGCTGTGTCCTT	1306
Db	401	ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu	420
QY	1307	AATCCAAATCTATATGGTTCTTAAATAATGGGATTAAAGCTGATTTAGTGTCCCTTATA	1366
Db	421	AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuLeu	440
QY	1367	CACGTGCTTCATATG	1381
Db	441	HisCysLeuHisMet	445
RESULT 3			
ID	Q9GK73	PRELIMINARY; PRT; 445 AA.	
AC	Q9GK73		
DT	01-MAR-2001	(TREMBLrel. 16, Created)	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE	Neuropeptide Y receptor Y5		
OS	Macaca mulatta (Rhesus macaque)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecoidea; Macaca		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21184974; PubMed=11287088;		
RA	Gehlert D.R., Yang P., George C., Wang Y., Schober D.,		
RA	Gackenhelmer S., Johnson D., Beavers L.S., Gadski R.A., Baez M.;		
RT	"Cloning and characterization of Rhesus monkey neuropeptide Y receptor		
RT	subtypes(1).";		
RL	Peptides 22:343-350(2001).		
DR	EMBL; AF303091; AAG40773.1; ..		
DR	GO; GO:0046021; C:integral to membrane; IEA.		
DR	GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR	GO; GO:0007218; P:neuropeptide signaling pathway; IEA.		
DR	InterPro; IPR000276; GPCR_Rhodopsn		
DR	InterPro; IPR000393; NPY5_Receptor.		
DR	InterPro; IPR000611; NPY_Receptor.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PRINTS; PR01016; NRPEPTIDEYR.		
DR	PRINTS; PR01012; NRPEPTIDEYR.		
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.		
KW	Neuropeptide; Receptor		
SQ	SEQUENCE 445 AA; 50812 MW; ASDACD259675BC93 CRC64;		
Alignment Scores:			
Pred. No.:	9.17e-183	Length:	445
Score:	2318.00	Matches:	442
Percent Similarity:	99.78%	Conservative:	2
Best Local Similarity:	99.33%	Mismatches:	1
Query Match:	93.47%	Indels:	0
DB:	2	Gaps:	0
US-09-771-956-4 (1-1406) x Q9GK73 (1-445)			
QY	47	ATGATTTAGAGCTCGACGAGTATTATAAAGACACTTGGCCAGAGATAATACGTCT	106
Db	1	MetAspLeuGluLeuAspGluTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla	20
QY	107	GCCACTCGGAATTCGATTTCCGAGTCTGGGATGACTATAAACGAGTGTAGTACTTA	166

Db	21	AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu	40
QY	167	CAGTATTTCTGATGGGCTCATACATTTGTAGTCTCTTGGCTTTATGGGNAATCTA	226
Db	41	GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu	60
QY	227	CTTATTTAATGGCTCTCATGAAAGCGTAATCAGAAGACTACGGTAAACTTCTCAT	286
Db	61	LeuLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuLeu	80
QY	287	GGCAATCTGGCCCTTTCTCATATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	346
Db	81	GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr	100
QY	347	TCTGTCTCTCGATCAGTCAGTGGATGTTTGGCAAGTCATGTCCATATATATATAT	406
Db	101	SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisLeuMetProPheLeu	120
QY	407	CAATGTGTCTCAGT	466
Db	121	GlnCysValSerValLeuValSerThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	140
QY	467	CATATGATAAATCATCCCATATCTTAATTAATTAACAGCAACCATGGTACTTCTGATA	526
Db	141	HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu	160
QY	527	GCTACTGTCTGGACACTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	586
Db	161	AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu	180
QY	587	GTGGAACTTCAAGAAACATTTGGTTCAGCATTTGCTGACAGCAGGATATTATGTTGAG	646
Db	181	ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu	200
QY	647	TCATGGCCATCTGATTTCATACAGAAATTCCTTACTATCTCTTTATTCTAGTTCAGTAT	706
Db	201	SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuLeuValGlnTyr	220
QY	707	ATTCTGCCCTTAGTTTGTCTTACTTAAGTCATACAACTGTCTGCAAGATATAGCTGT	766
Db	221	IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys	240
QY	767	CGATTGTCCAAAGAAACAGACTTCAAGAAATAGATGATCACTTAACCTTCTTCTCAT	826
Db	241	GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis	260
QY	827	CCATCCAAAAGAGTGGGCTCAGTGAAACTCTCTGGCAGCCATAAATGAGGATTATCA	886
Db	261	ProSerArgLysIleGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer	280
QY	887	TTTCATCAAAAACACAGAGAAGATATAGCAAGACAGCATGTGTGTACCTGCTTCA	946
Db	281	PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro	300
QY	947	GAAGACCTTCTCAAGAGAACACCTCCAGATACTTCCAGAAAACCTTTGGCTCTGTAGA	1006
Db	301	GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg	320
QY	1007	AGTCAGCTCTCTTCATCCAGTAAGTTCATACCAGGGGTCCTTGTGTGAGTAAAA	1066
Db	321	SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluLeuLys	340
QY	1067	CCTGAAGAAAATTCAGATGTTTCATCAATTGAGAGTAAACGTTCTGTGTACAGAAATAAA	1126
Db	341	ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys	360
QY	1127	AAGAGATCTCGAAGTGTCTTCTACAGCTGACCATCTGATATAGTATTGCTGTGTAGT	1186
Db	361	LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer	380
QY	1187	TGGATGCCACTACACTTTTCCATGTGTAAGTATTTAATGACAACTTTATTTCAAAT	1246
Db	381	TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuLeuSerAsn	400

QY 1247 AGGATTCAGTTGGTGTATGATTTGATTTGATTTGGTCATGATGCTGCTGTGCTT 1306
 Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 420
 QY 1307 AATCCAATTCATATAGTTTCTTAATAATGGGATTAAAGCTGATTTAGTGCTCCCTTATA 1366
 Db 421 AsnProLeuLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuMetSerLeu 440
 QY 1367 CACTGCTTCATATG 1381
 Db 441 HisCysLeuHisMet 445

RESULT 4
 Q925F1 PRELIMINARY; PRT; 446 AA.
 AC Q925F1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NPV receptor 5.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21184976; PubMed=11287090;
 RX Lundell I., Eriksson H., Marklund U., Larhammar D.;
 RT "Cloning and characterization of the guinea pig neuropeptide Y
 receptor Y5.";
 RL Peptides 22:357-363(2001).
 DR EMBL; AF363240; AAK52800.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000393; NPV5_receptor.
 DR InterPro; IPR000611; NPV_receptor.
 DR Pfam; PF00001; 7cm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01016; NRPEPTIDEY5R.
 DR PRINTS; PR01012; NRPEPTIDEYR.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 446 AA; 50936 MW; 2C3984B0A90AA693 CRC64;

Alignment Scores:
 Pred. No.: 2.1e-176 Length: 446
 Score: 2241.00 Matches: 446
 Percent Similarity: 97.75% Conservative: 10
 Best Local Similarity: 95.51% Mismatches: 10
 Query Match: 90.36% Indels: 0
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x Q925F1 (1-446)

QY 47 ATGGATTAGAGCTCGAGAGTATTATAAAGACACTTGGCCAGAGATAATACTGCT 106
 Db 1 MetAspLeuGluLeuLysGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrThr 20
 QY 107 GCCACTCGGAATTCGATTTCCAGCTCGGATGACATATAAAGACGTGTAGATGACTTA 166
 Db 21 ThrThrArgAsnSerAspPheProValTyrAspAspTyrArgSerSerValAspLeu 40
 QY 167 CAGTATTTTCATGGGCTATACATTTGTAGTCTCTTGGCTTATGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 QY 227 CTTATTTTAAATGGTCTCATGAAAAGCGTAATCAGAAGACTACGGTAAACTTCCTCAT 286

Db 61 LeuIleLeuMetAlaLeuIleLysLysArgAsnGlnLysThrThrValAsnPheLeuIle 80
 QY 287 GGCATCTCGCTTTTCTGATATCTTGTTGCTGCTTTTGTCTCACCTTTTCACACTGAGC 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGCTCTCTGATCAGTGGATTTGGCAAGTCATGTCGCATATATATGCTCTTTCTT 406
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
 QY 407 CAATGTGTCTCAGTTTGGTTTCAACTTTAAATTTAATATCAATTGCCATTTCCAGGTAT 466
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
 QY 467 CATATGATAAATCAATCCCATATCTAATAATTAACAGCAACCATGGCTACTTCTGATA 526
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
 QY 527 GCTACTGTCTGGACACTAGTTTTCATCTCTTCCCTTCCAGTGTTCACAGTCTT 586
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
 QY 587 GTGGAACTTCAAGAAACATTTGGTTTCAGATTTGCTGAGCAGCAGGTATTTATGTTGAG 646
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
 QY 647 TCATGGCCATCTGATTCATACAGAAATTCCTTTACTATCTCTTTTGTAGTCTCAGTAT 706
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
 QY 707 ATTCTGCCCTTAGTTGTCTTACTAGTCTATACAAAGTGTCTGCAGAAAGTATAGCTGT 766
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
 QY 767 GGATTTGTCACAAAGAAACAGACTTGAAGAAATAGATCATCAACTTACTCTTCAT 826
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
 QY 827 CCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCAATAAATGGAGTTATTC 886
 Db 261 ProSerLysLysSerGlyAsnGlnValLysLeuSerLysThrHisLysTrpSerTyrSer 280
 QY 887 TTCATCAAAAAACACAGAAAGATATAGCAGAGACAGACATGTGTCTTACTCTCTCCA 946
 Db 281 PheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
 QY 947 GAAAGACCTTCTCAAGAGAACCACTCCAGATACCTTCCAGAAAACCTTTGGCTCTGTA 1006
 Db 301 AlaArgProSerLeuGluAsnGlnSerArgThrLeuProGluAsnPheGlySerValArg 320
 QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACCAGGGGTCCCACTTGTCTTGAGATAAAA 1066
 Db 321 SerGlnIleSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
 QY 1067 CCTGAAGAAATTCAGATGTTTCATGAATTCAGAGTAAACCGTCTGTTCACAGAAATAAAA 1126
 Db 341 ProGluAspAsnSerAspAlaHisGluMetArgValLysArgSerIleThrArgIleLys 360
 QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATTAATGATTTCTGTACT 1186
 Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleValPheAlaValSer 380
 QY 1187 TGGATGCCACTACACCTTTTCCATGCTGTAAGTATTAATGACAACTTTATTTCAAT 1246
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400
 QY 1247 AGGCATTTTCAAGTGTGTATTCATTTCTATTGTTGGGATGATGTCCTGTGTCTT 1306
 Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 420
 QY 1307 AATCCAATTCATATGGGTTTCTTAATAATGGGATTAAGAGCTGATTTAGTCTCCTTATA 1366
 Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuMetSerLeuIle 440

QY 1367 CACTGTCTTCATATG 1381
 DB 441 HisCysLeuHisLeu 445

RESULT 5
 NY5R CANFA STANDARD; PRT; 446 AA.
 AC 062729;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor) (NPY5)
 GN Name=NPY5R; Synonyms=NPY5;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_taxid=9615;
 RN [1]
 RZ SEQUENCE FROM N.A.
 RX MEDLINE=99017379; PubMed=9802393;
 RA Bowsley B., Walker M.W., Bard J., Weinshank R.L., Laz T.M.,
 RA Vaynsky P., Branchek T.A., Gerald C.;
 RT "Molecular biology and pharmacology of multiple NPY Y5 receptor species homologs";
 RL Regul. Pept. 75:45-53 (1998).
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity. Seems to be associated with food intake. Could be involved in feeding disorders (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Highest to tachykins receptors.

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 DR EMBL; AF049328; AAC17838.1; .
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000393; NPY5_receptor.
 DR InterPro; IPR000611; NPY_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation; Transmembrane.
 KW DOMAIN 1 40 Extracellular (Potential).
 FT TRANSMEM 41 62 1 (Potential).
 FT DOMAIN 63 74 Cytoplasmic (Potential).
 FT TRANSMEM 75 95 2 (Potential).
 FT DOMAIN 96 115 Extracellular (Potential).
 FT TRANSMEM 116 137 3 (Potential).
 FT DOMAIN 138 157 Cytoplasmic (Potential).
 FT TRANSMEM 158 178 4 (Potential).
 FT DOMAIN 179 210 Extracellular (Potential).
 FT TRANSMEM 211 232 5 (Potential).
 FT DOMAIN 233 368 Cytoplasmic (Potential).
 FT TRANSMEM 369 391 6 (Potential).
 FT DOMAIN 392 404 Extracellular (Potential).
 FT TRANSMEM 405 428 7 (Potential).
 FT DOMAIN 429 446 Cytoplasmic (Potential).
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (Potential).
 FT DISULFID 114 198 By similarity.
 FT LIPID 442 442 S-palmitoyl cysteine (Potential).
 SQ SEQUENCE 446 AA; 51012 MW; 5CAC8D2FCF5D254A CRC64;

Alignment Scores: 3.01e-175 Length: 446
 Pred. No.: 2227.00 Matches: 422
 Percent Similarity: 97.30% Conservative: 11
 Best Local Similarity: 94.83% Mismatches: 12
 Query Match: 89.80% Indels: 0
 DB: 1 Gaps: 0

US-09-771-956-4 (1-1406) x NY5R_CANFA (1-446)

QY 47 ATCGATTAGAGCTCGACGAGTATTATACAGACACTTGCACAGAGAAATAACTGCT 106
 DB 1 MetAspLeuGluGlnAspPheYrAsnLysThrLeuAlaThrGluAsnThrAla 20
 QY 107 GCACCTCGGAATTCGATTCCCACTCTGGGATGACTATAAAGCAGGTGTAGATGACTTA 166
 DB 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
 QY 167 CAGTATTTCTGATTGGGCTCTATACATTCTGAATCTTCTTGGCTTTATGGGAATCTA 226
 DB 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 QY 227 CTTATTTTAATGGCTCTCATGAAAGGCTAATCAGAAAGACTACGGTAAACTTCTCATA 286
 DB 61 LeuIleLeuMetAlaLeuMetArgLysArgAsnGlnLysThrMetValAsnPheLeuIle 80
 QY 287 GGCATCTGGCCTTTCTGATATCTTGGTTGCTGCTGTTTGTCTACCTTTCACACTGAG 346
 DB 81 GlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGCTCTGCTGATCAGTGGATGTTTGGCAAGTCATGTGCCATATTATGCTTTTCTT 406
 DB 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
 QY 407 CAATGTGTCTAGTTTGGTTTCAACTTAATTTAATCAATTCGCAATTCGCTAGGTAT 466
 DB 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
 QY 467 CATATGATAAATCCCATATCTAATTAATTTAACAGCAAAACCATGCTTCTTGATA 526
 DB 141 HisMetIleLysHisProIleSerAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
 QY 527 GCTACTGTCTGGACACTAGTGTTCCTCCATCTGTTTCCCTTCCAGTGTTCACAGTCTT 586
 DB 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
 QY 587 GTGGAACTTCAGAAACATTTGGTTCAGCATGCTGACGACAGGTATTATGTTGTCAG 646
 DB 181 ValGluLeuGlnGluThrPheAspSerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
 QY 647 TCATGGCCATCTGATTTCATACAGAAATTCCTTACTATCTCTTTATTCCTAGTTCAGTAT 706
 DB 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
 QY 707 ATTCGCCCTTAGTTTGTCTTACTGTAGTCTATCAAGTGTCTGACAGATATAGCTGT 766
 DB 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
 QY 767 GGATTGTCCCAACAAAGAAAACAGACTTGAAGAAATAGATGATCAACTTAACCTTTCAT 826
 DB 241 GlyLeuSerAsnLysGluAsnLysLeuGluGluAsnGluMetIleAsnLeuThrLeuGln 260
 QY 827 CCATCCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCATAAATGAGATTATCA 886
 DB 261 ProPheLysLysSerGlyProGlnValLysLeuSerSerHisLysLysTrpSerTyrSer 280
 QY 887 TTCATCAAAAACACAGAGAGATATAGCAAGAGACAGCATGTGTGTACCTGCTCCA 946
 DB 281 PheIleArgLysHisArgArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
 QY 947 GAAAGACCTTCTCAAGAGAACCACTCCAGAATACTCCAGAAAACCTTGGCTCTCTAAGA 1006

Db 301 AlaArgProGlnGluAsnHisSerArgMetLeuProGluAsnPheGlySerValArg 320
 Qy 1007 AGTCAGCTCTTCATCCAGTAAGTTCATACCCAGGGTCCCACTGCTTGTGATATAA 1066
 Db 321 SerGlnHisSerSerSerLysPheIleProGlyValProThrCysPheGluValLys 340
 Qy 1067 CCTGAAGAAAATTCAGATGTTTCATGATTCAGAGTAAACGCTCTGTTCACAGATAAAA 1126
 Db 341 ProGluGluAsnSerAspValHisAspMetArgValAsnArgSerIleMetArgIleLys 360
 Qy 1127 AAGAGATCTCGAAGTGTTCCTACAGACTGACACTGATGATATAGTATTTGCTGTAGT 1186
 Db 361 LysArgSerArgSerValPheTyArgLeuThrIleLeuLeuValPheAlaValSer 380
 Qy 1187 TGGATGCCACTACACCTTTTCCATGCTGTAAGTATTTTAAATGACAACTCTATTTCAAAT 1246
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspLeuIleSerAsn 400
 Qy 1247 AGGCATTTCAAGTTGGTGTATTGTCATTTGTCATTTGTTGGCATGATGTCCTGTGCTT 1306
 Db 401 ArgHisPheLysLeuValTyrcysileCysHisLeuLeuGlyMetMetSerCysLeu 420
 Qy 1307 AATCCATTCATATGAGTGTCTTCTTAATTAATGGGATTAAGCTGATTTAGTGTCCCTATA 1366
 Db 421 AsnProIleuTyArgPheLeuAsnAsnGlyIleLysAlaAspLeuIleSerLeu 440
 Qy 1367 CACTGTCTTCATATG 1381
 Db 441 GlnCysLeuHisMet 445

RESULT 6
 NYSR_RAT
 ID NYSR_RAT STANDARD; PRT; 456 AA.
 AC Q63634; P70586;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY-5) (NPY-5 receptor) (Y5 receptor).
 GN Name=Npy5r; Synonyms=NPY5;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 (1)
 RN Neuropeptide Y receptor type 5 (NPY-5) (NPY-5 receptor) (Y5 receptor).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=963117589; PubMed=8700207;
 RA Gerald C., Walker M.W., Criscione L., Gustafson E.L.,
 RA Batzl-Hartmann C., Smith K.E., Vayse P., Durkin M.M., Laz T.M.,
 RA Linemeyer D.L., Schaffhauser A.O., Whitebread S., Hofbauer K.G.,
 RA Taber R.I., Branchek T.A., Weinschenk R.B.;
 RT "A receptor subtype involved in neuropeptide-Y-induced food intake."
 RL Nature 382:168-171(1996).
 (2)
 RN Neuropeptide Y receptor type 5 (NPY-5) (NPY-5 receptor) (Y5 receptor).
 RP SEQUENCE OF 12-456 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=9631165; PubMed=9659502;
 RA Parker E.M., Babij C.K., Balasubramanian A., Burrier R.E., Guzzi M.,
 RA Hamud F., Mukhopadhyay G., Rudinski M.S., Tao Z., Tice M., Xia L.,
 RA Mullins D.E., Salisbury B.G.;
 RT "GR231118 (1229U91) and other analogues of the C-terminus of
 RT neuropeptide Y are potent neuropeptide Y Y1 receptor antagonists and
 RT neuropeptide Y Y4 receptor agonists."
 RL Eur. J. Pharmacol. 349:97-105(1998).
 (3)
 RN Neuropeptide Y receptor type 5 (NPY-5) (NPY-5 receptor) (Y5 receptor).
 RP SEQUENCE OF 12-456 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96421636; PubMed=8824284;
 RA Hu Y., Bloomquist B.T., Cornfield L.J., Decarr L.B.,
 RA Flores-Riveros J.R., Friedman L., Jiang P., Lewis-Higgins L.,
 RA Sadowski Y., Schaefer J., Velazquez N., McCabe M.L.;
 RT "Identification of a novel hypothalamic neuropeptide Y receptor

RT associated with feeding behavior.";
 RL J. Biol. Chem. 271:26315-26319(1996).
 CC !- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity
 CC of this receptor is mediated by G proteins that inhibit adenylate
 CC cyclase activity. Seems to be associated with food intake. Could
 CC be involved in feeding disorders.
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.
 CC !- TISSUE SPECIFICITY: Brain; hypothalamus.
 CC !- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Highest to tachykinins receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U56078; AAC52677.1; -;
 CC EMBL: AF044264; AAC15670.1; -;
 CC EMBL: U62674; AAC52845.1; -;
 CC RGD: 3199; NPY5r.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC InterPro: IPR000393; NPY5_receptor.
 CC InterPro: IPR000611; NPY_receptor.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS: PR00237; GPCR_RHODOPSIN.
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 CC PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Phosphorylation; Transmembrane.
 FT DOMAIN 1 51 Extracellular (Potential).
 FT TRANSMEM 52 73 1 (Potential).
 FT DOMAIN 74 85 Cytoplasmic (Potential).
 FT TRANSMEM 86 106 2 (Potential).
 FT DOMAIN 107 126 Extracellular (Potential).
 FT TRANSMEM 127 148 3 (Potential).
 FT DOMAIN 149 168 Cytoplasmic (Potential).
 FT TRANSMEM 169 189 4 (Potential).
 FT DOMAIN 190 221 Extracellular (Potential).
 FT TRANSMEM 222 243 5 (Potential).
 FT DOMAIN 244 378 Cytoplasmic (Potential).
 FT TRANSMEM 379 401 6 (Potential).
 FT DOMAIN 402 414 Extracellular (Potential).
 FT TRANSMEM 415 438 7 (Potential).
 FT DOMAIN 439 456 Cytoplasmic (Potential).
 FT DISULFID 125 209 By similarity.
 FT LIPID 452 452 S-palmitoyl cysteine (Potential).
 FT CARBOHYD 21 21 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 456 AA; 51715 MW; 5157ABE341BA707E CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 1,78e-163 Length: 456
 Score: 2084.50 Matches: 396
 Percent Similarity: 93.10% Conservative: 22
 Best Local Similarity: 88.20% Mismatches: 30
 Query Match: 84.05% Indels: 1
 DB: 1 Gaps: 1
 US-09-771-956-4 (1-1406) x NY5R_RAT (1-456)
 Qy 35 CAGGACTATAATGAGTTAGAGTCGACGAGTATTATAACAAGACACTGCCACAGAG 94
 Db 8 GlnAspSerSerMetGluPheLysLeuGluHisPheAsnLysThrPheValThrGlu 27
 Qy 95 AATAATACCTGCGCCACTCGGAATCTGATTTCCAGCTCGGATGACTATAAAGCACT 154
 Db 28 AsnAsnThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 47
 Qy 155 GTAGATGACTTACAGTATTTCTGATTTGGCTCTTACATTTGTAAGTCTTCTTGCTTT 214

DR PRINTS; PRO0237; GPCRHOOPS.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; FALSE_NEG.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Phosphorylation; Transmembrane
 FT DOMAIN 1 61 Extracellular (Potential).
 FT TRANSMEM 62 83 1 (Potential).
 FT DOMAIN 84 95 Cytoplasmic (Potential).
 FT TRANSMEM 96 116 2 (Potential).
 FT DOMAIN 117 136 Extracellular (Potential).
 FT TRANSMEM 137 158 3 (Potential).
 FT DOMAIN 159 178 Cytoplasmic (Potential).
 FT TRANSMEM 179 199 4 (Potential).
 FT DOMAIN 200 231 Extracellular (Potential).
 FT TRANSMEM 232 253 5 (Potential).
 FT DOMAIN 254 388 Cytoplasmic (Potential).
 FT TRANSMEM 389 411 6 (Potential).
 FT DOMAIN 412 424 Extracellular (Potential).
 FT TRANSMEM 425 448 7 (Potential).
 FT DOMAIN 449 466 Cytoplasmic (Potential).
 FT DISULFID 135 219 By similarity.
 FT LIPID 462 462 S-palmitoyl cysteine (Potential).
 FT CARBOHYD 10 10 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 17 17 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 38 38 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 39 39 N-linked (GLCNAC. .) (Potential).
 FT CONFLICT 195 195 L -> P (in Ref. 1).
 FT CONFLICT 284 284 K -> Q (in Ref. 3).
 SQ SEQUENCE 466 AA; 52784 MW; B157F236EF24385 CRC64;

Alignment Scores:

Pred. No.: 2,8e-162 Length: 466
 Score: 2070.00 Matches: 397
 Percent Similarity: 90.13% Conservative: 23
 Best Local Similarity: 85.19% Mismatches: 24
 Query Match: 83.47% Indels: 22
 DB: 1 Gaps: 2

US-09-771-956-4 (1-1406) x NYSR_MOUSE (1-466)

QY 47 ATGATTTAGAGTCGACGAGTATTATACAGACACTTCCACAGAGATATATCTGCT 106
 Db 1 MetGluValLysLeuGluHisPheAsnLysThrPheValThrGluAsnAsnThrAla 20
 QY 107 GCCACT----- 112
 Db 21 AlaSerGlnAsnThrAlaSerProAlaTrpGluAspTyrArgGlyThrGluAsnAsnThr 40
 QY 113 -----CGGAATTCGTATTTCCAGTCTGGGATGACTATATAAAGCAGCTAGATGAC 163
 Db 41 SerAlaAlaArgAsnThrAlaPheProValTrpGluAspTyrArgGlySerValAspAsp 60
 QY 164 TTACAGTATTTCTGATGGCTCTATACATTTGTAGTCTTCTGGCTTTATGGGAAT 223
 Db 61 LeuGlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsn 80
 QY 224 CTACTTTATTTTAAATGGCTCTCATGAAAGCGTAATCAGAGACTACGGTAAACTTCCTC 283
 Db 81 LeuLeuLeuLeuMetAlaValMetLysLysArgAsnGlnLysThrThrValAsnPheLeu 100
 QY 284 ATAGCAATCTGGCTTTCTGATATCTTGGTGTGCTGTGCTTCTGCTCACCCTTCACACTG 343
 Db 101 IleGlyAsnLeuAlaPheSerAspIleLeuValValLysPheCysSerProPheThrLeu 120
 QY 344 ACGTCTGCTGCTGGATGATGATGTTGGCAAGTCTATGTCATATATATGTCCTTTT 403
 Db 121 ThrSerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPhe 140
 QY 404 CTTCAATGTGCTCAGTTTGGTTTCAACTTAAATTAATATATCAATGTCATGTCAGG 463
 Db 141 LeuGlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArg 160
 QY 464 TATCATATGATAAACAATCCCATATCTATATATTTACAGCAACCATGGCTACTTCTG 523

Db 161 TyrHisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeu 180
 QY 524 ATAGTACTGTCTGGACACTAGTTTTCGCCATCTGTTCCCTCCCTCCAGTGTTCACAGT 583
 Db 181 IleAlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSer 200
 QY 584 CTTGTGNACTTCAAGAAACATTTGGTTTTCAGCATTGCTGAGCAGCAGGATTTATGTGT 643
 Db 201 LeuValGluLeuLysGluThrPheGlySerAlaLeuLeuSerSerLysTyrLeuCysVal 220
 QY 644 GAGTCATGGCCATCTGATTTCATACAGAAATTCCTTTTACTATCTCTTATTGCTAGTTCAG 703
 Db 221 GluSerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGln 240
 QY 704 TATATTGCTGCTTGTAGTTTGTCTTACTGTAAGTCTATCAAGTCTGTCAGAGATATAAGC 763
 Db 241 TyrIleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSer 260
 QY 764 TGTGATTTGTCACAAAGAAACAGACTTCAAGAAATGAGATGATCAACTTAACTCTT 823
 Db 261 CysGlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeu 280
 QY 824 CATCCATCCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGCGACGCCATAAATGAGTAT 883
 Db 281 HisProSerLysLysSerArgAspGlnAlaLysProProSerThrGlnLysTrpSerTyr 300
 QY 884 TCATTTCATCAAAACACAGAGAGATATAGCAAGAGACAGATGCTGTCTTACTCTCT 943
 Db 301 SerPheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAla 320
 QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATATCTCCAGAAACCTTTGGCTCTCTA 1003
 Db 321 ProAlaGlyProSerGlnGluLysHisLeuThrVal---ProGluAsnProGlySerVal 339
 QY 1004 AGAAGTCACTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTGTCTTCAGATA 1063
 Db 340 ArgSerGlnLeuSerProSerLysValIleProGlyValProIleCysPheGluVal 359
 QY 1064 AAACCTGGAAGAAATTCAGATGTTTCATGAATTCAGAGTAAACCTTCTGTACAGAATA 1123
 Db 360 LysProGluGluSerSerAspAlaGlnGluMetArgValLysArgSerLeuThrArgile 379
 QY 1124 AAAAGAGATCTCGAAGTGTCTTTCACAGACTGACCATCTGATATAGTATTTGCTCTT 1183
 Db 380 LysLysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaVal 399
 QY 1184 AGTTGATGCCACTACACTTTTCCATGTTGGTAACTGATTTTAATGACAACTTTATTTCA 1243
 Db 400 SerTrpMetProLeuHisValPheHisValThrAspPheAsnAspAsnLeuIleSer 419
 QY 1244 AATAGGCATTTCAAGTGTGTTGATTCATTTGTCATTTGTTGGGATGATGTCCTGTTGT 1303
 Db 420 AsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetSerCysCys 439
 QY 1304 CTTATCCAACTCTATATGGTTCCTTAATATGGGATTAAGCTGATTAGTGTCCCTT 1363
 Db 440 LeuAsnProIleLeuTyrGlyPheLeuAsnGlnGlyIleLysAlaAspLeuArgAlaLeu 459
 QY 1364 ATACACTGCTCTCATATG 1381
 Db 460 IleHisCysLeuHisMet 465
 RESULT 8
 BAC32426 PRELIMINARY; PRT; 466 AA.
 ID BAC32426
 AC BAC32426;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Adult male corpora quadrigemina cDNA, RIKEN full-length enriched
 DE library, clone:B230213K17 product:NEUROPEPTIDE Y RECEPTOR TYPE 5, full
 DE insert sequence.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=22354683; PubMed=12466851;
 RA THE FANTOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RA Kono H., Okazaki Y., Muramatsu M., Sugahara Y., Shibata K., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN (6)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Iwama M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN (6)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuo M., Hasegaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AK045587; BAC32426.1;
 KW Neuropeptide; Receptor.
 SQ SEQUENCE 466 AA; 52784 MW; B157F236EF2D4385 CRC64;

Alignment Scores:

Pred. No.: 2,8e-162 Length: 466
 Score: 2070.00 Matches: 397
 Percent Similarity: 90.13% Conservative: 23

Best Local Similarity: 85.19% Mismatches: 24
 Query Match: 83.47% Indels: 22
 DB: 2 Gaps: 2
 US-09-771-956-4 (1-1406) x BAC32426 (1-466)
 QY 47 ATGGATTAGACTCGAGAGTATTATACAGACACTTGCACAGAGAAATAACTGCT 106
 DB 1 MetGluValLysLeuGluGluHisPheAsnLysThrPheValThrGluAsnAsnThrAla 20
 QY 107 GCCACT----- 112
 DB 21 AlaSerGlnAsnThrAlaSerProAlaTrpGluAspTyrArgGlyThrGluAsnAsnThr 40
 QY 113 -----CGGAATTCCTGATTCCTCCAGTCTGGGATGACTATAAAGCAGGTGATGAC 163
 DB 41 SerAlaAlaArgAsnThrAlaPheProValTrpGluAspTyrArgGlySerValAspAsp 60
 QY 164 TTACAGTATTTCTGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAAAT 223
 DB 61 LeuGlnTyrPheLeuLeuGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsn 80
 QY 224 CTACTTATTTAATCGCTCTCATGAAAGCGTATATCAGAAAGCTACGCTAAACTTCCTC 283
 DB 81 LeuLeuLeuLeuMetAlaValMetLysLysArgAsnGlnLysThrThrValAsnPheLeu 100
 QY 284 ATAGCAATCTGGCCTTTCTGATATCTGTTGCTGTTGCTGTTGCTGCTACCTTTACACTG 343
 DB 101 IleGlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerProPheThrLeu 120
 QY 344 AGCTCTGCTCTCGATCGATGGATGTTTGGCAAGTCATGTCCTATATATGCTTTT 403
 DB 121 ThrSerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPhe 140
 QY 404 CTTCAATGTGTGCTCAGTTTGGTTTCACTTTAATTTAATATATCAATTCCTGCTGAG 463
 DB 141 LeuGlnCysValSerValLeuValSerThrLeuIleLeuSerIleAlaIleValArg 160
 QY 464 TATCATATGATAAATCATCCATATCTAATAATTTACAGCAACCATGGCTACTTCTG 523
 DB 161 TyrHisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeu 180
 QY 524 ATAGCTACTGTCTGGACACTAGGTTTGGCAATCTGTTCTCCCTTCCAGTGTTCACAGT 583
 DB 181 IleAlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSer 200
 QY 584 CTTGTGGAACCTCAAGAAACATTTGGTTCACCATGCTGAGCAGCAGGATTTATGTT 643
 DB 201 LeuValGluLeuLysGluThrPheGlySerAlaLeuLeuSerSerLysTyrLeuCysVal 220
 QY 644 GAGTCATGGCCATCTGATTCATACAGAAATTCCTTCTTACTTCTTATTCCTGAGTTCAG 703
 DB 221 GluSerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGln 240
 QY 704 TATATTCGCCCTTAGTGTTCCTTACTGTAAGTCATACAAAGTGTCTGCAGAGTATAGC 763
 DB 241 TyrIleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSer 260
 QY 764 TGTGATTGTCCAAAGAAACAGACTTGAAGAAATGAGATGATCAACTTAACCTT 823
 DB 261 CysGlyLeuSerHisLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeu 280
 QY 824 CATCATCAAAAAAGAGTGGCCTCAGGTGAACTCTCTGCGAGCCCAATAATGAGGTAT 883
 DB 281 HisProSerLysLysSerArgAspGlnAlaLysProSerThrGlnLysTrpSerTyr 300
 QY 884 TCATTTCATCAAAAAACACAGAGAGATATAGCAGAGACAGCATGTGTTGCTACCTGCT 943
 DB 301 SerPheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAla 320
 QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATATCTCCAGAAACTTTGGCTCTGTA 1003
 DB 321 ProAlaGlyProSerGlnGluLysHisLeuThrVal---ProGluAsnProGlySerVal 339

QY 1004 AGAAGTCAGCTCTCTCATCAGTAAGTTCATACGAGGGTCCCACTGCTTGCAGATA 1063
 Db 340 AGSserGlnLeuSerProSerSerLysValIleProGlyValPcoileCysPheGluVal 359
 QY 1064 AAACCTGAAGAAATTCAGATGTTTCATGAATGAGAGTAAACGTTCTGTACAGATA 1123
 Db 360 LysProGluGluSerSerAspAlaGlnGluMetArgValLysArgSerLeuThrArgile 379
 QY 1124 AAAAGAGATCTCGAAGTGTTCCTACAGACTGCCATCTGATATAGTATGCTGTT 1183
 Db 380 LysLysArgSerArgSerValPheYrArgLeuThrIleLeuIleLeuValPheAlaVal 399
 QY 1184 AGTTGATGCCACTACACTTCCATGCTGTAATGATGTTTAAATGACAACTTATTCA 1243
 Db 400 SerTrpMetProLeuHisValPheHisValThrAspPheAsnAspLeuIleSer 419
 QY 1244 ATAGGCAATTCAGCTGGTGTATGCTATGTCATTTGTCATTTGGCAGTGTCTGTTGT 1303
 Db 420 AsnArgHisPheLysLeuValYrCysIleCysHisLeuLeuGlyMetMetSerCysCys 439
 QY 1304 CTTAATCCAAATCTATATGGGTTCTTAATATGGGATTAAGCTGATTTAGTGTCCCTT 1363
 Db 440 LeuAsnProIleLeuTyGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeu 459
 QY 1364 ATACACTGCTTCATATG 1381
 Db 460 IleHisCysLeuHisMet 465

RESULT 9
 NY5R_PIG
 ID NY5R_PIG STANDARD; PRT; 446 AA.
 AC 097959;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Neuropeptide Y receptor type 5 (NPY5-R) (NPY-Y5 receptor) (Y5 receptor).
 DE receptor.
 GN Name=NPY5R; Synonyms=NPYR5;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P.,
 RA Andersson L., Lathammar D.;
 RT "porcine NPY receptors NPY1R, NPY2R and NPY5R: cloning, mapping and
 RT comparative analysis";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LWD; TISSUE=Kidney;
 RA Ito Y., Minezawa M.;
 RT "Sus scrofa gene for neuropeptide Y receptor type 5, complete cds.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for neuropeptide Y and peptide YY. The activity
 CC of this receptor is mediated by G proteins that inhibit adenylyate
 CC cyclase activity. Seems to be associated with food intake. Could
 CC be involved in feeding disorders (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Highest to tachykinins receptors.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF106093; AAD13778.1; -

DR EMBL; AB019185; BAA34055.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000393; NPY5_receptor.
 DR InterPro; IPR000611; NPY_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KW Phosphorylation; Transmembrane.
 KW DOMAIN 1 40 Extracellular (Potential).
 FT TRANSMEM 41 62 1 (Potential).
 FT DOMAIN 63 74 Cytoplasmic (Potential).
 FT TRANSMEM 75 95 2 (Potential).
 FT DOMAIN 96 115 Extracellular (Potential).
 FT TRANSMEM 116 137 3 (Potential).
 FT DOMAIN 138 157 Cytoplasmic (Potential).
 FT TRANSMEM 158 178 4 (Potential).
 FT DOMAIN 179 210 Extracellular (Potential).
 FT TRANSMEM 211 232 5 (Potential).
 FT DOMAIN 233 368 Cytoplasmic (Potential).
 FT TRANSMEM 369 391 6 (Potential).
 FT DOMAIN 392 404 Extracellular (Potential).
 FT TRANSMEM 405 428 7 (Potential).
 FT DOMAIN 429 446 Cytoplasmic (Potential).
 FT CARBOHYD 10 10 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 17 17 N-linked (GlcNAc...) (potential).
 FT DISULFID 114 198 By similarity.
 FT LIPID 442 442 S-palmitoyl cysteine (Potential).
 SQ SEQUENCE 446 AA; 50474 MW; B7F616C394C6CA0 CRC64;

Alignment Scores:

Pred. No.: 8,24e-159 Length: 446
 Score: 2028.00 Matches: 380
 Percent Similarity: 93.03% Conservatives: 34
 Best Local Similarity: 85.39% Mismatches: 31
 Query Match: 81.77% Indels: 0
 DB: 1 Gaps: 0

US-09-771-956-4 (1-1406) X NY5R_PIG (1-446)

QY 47 ATGATTTAGAGCTCGAGAGTATTATAACAAGACACTTCCACAGAGATAATATCTGCT 106
 Db 1 MetGlySerGluIleProAspTyrAsnLysThrLeuAlaSerGluAsnAsnThrVal 20
 QY 107 GCACCTCGGAATTCGATTTCCCACTCTGGATGATCACTATAAAAGCAGTGTAGATGACTTA 166
 Db 21 AlaThrArgAsnSerGlyPheProValTrpGluAspTyrLysGlySerValAspAspLeu 40
 QY 167 CAGTATTTCTGATGGGCTCTATACATTTGTAGTCTTCTGGCTTTATGGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 QY 227 CTTATTTTAATGGCTCTCATGAAAACGTAATCAGAAGACTACGGTAAACTTCCTCATA 286
 Db 61 LeuIleLeuMetAlaValMetArgLysArgAsnGlnLysThrThrValAsnPheLeuIle 80
 QY 287 GCGAATCTGGCTTTCTCGATATCTTGGTGTGCTGTTTGTGCTTTCACCTTTCACACGACG 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGTTCTTGGGATCAGTGGATGCTTTGGCAAGTCAATGTCATATTATGCTCTTCTTCT 406
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
 QY 407 CAATGTGTGTCAGTTTGGTTTCAACTTTAATTTAATATCAATGCCATGTCAGGTAT 466
 Db 121 GlnCysValThrValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
 QY 467 CATATGATAAACATCCCATATCTTAATAATTTAACAGCAACCATGGCTACTTCTTGATA 526
 Db 141 HisMetIleLysHisProValSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160


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QY 647 TCATGCCCATCTGATTCATACAGAAATGGCTTTTACTATCTCTTTATGCTAGTTCAGTAT 706
Db 197 SerTyrProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuMetGlnTyr 216
QY 707 ATTCTGCCCTTACTTGTCTTACTGTAAGTCATACAGAGTGTCTGCAGAGTAACTGCT 766
Db 217 IleLeuProLeuValCysLeuThrAlaSerHisThrSerValCysArgSerValGlySer 236
QY 767 GGATTGTCCAAACAAAGAAACACAGCTTGAAGAAATGAGATGATCAACTTAATCTCTCAT 826
Db 237 ArgLeuSerSerLysGluGlyLysPheGlnGluAsnGluMetIleAsnLeuThrLeuHis 256
QY 827 CCATCCAAAGAGTGGGCTCAGGTCAAACTCTCTGGCAGCCATAAATGGAGTTATCCA 886
Db 257 ProSerLysSerAlaGlyThrGluAlaGlnProSerSerHisThrSerTyrSerCysAla 276
QY 887 TTCAATCAAAAACACAGAAAGATATAGCAAGAACACAGCATGTGTGTACCTGCTCCA 946
Db 277 LeuValArgLysHisHisArgGlySerLysLysThrSerThrValMetProAlaIle 296
QY 947 GAAGACCTCTCAAGAGAACCTCCAGATACATCTCCAGAAACCTTGGCTCTGTAAAGA 1006
Db 297 LeuArgGlnGlnGlnAspAlaAspPheArgAspLeuProGluThrSerGlyThrGluLys 316
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTGCTTTGAGATAAAA 1066
Db 317 SerGlnLeuSerSerSerSerLysPheIleProGlyValProIleCysPheGluMetLys 336
QY 1067 CCTGAAGAAATTCAGATGTCATGAA---TTGAGAGTAAACGTTCTGTGTACAGAAATA 1123
Db 337 ProGluGluAsnThrGluGlnAspMetIleThrValSerGlnSerIleIleArgIle 356
QY 1124 AAAAGAGATCTCGAAGTGTCTTACAGACTGACCATCTGATATAGTATTTGCTGTT 1183
Db 357 LysThrArgSerArgValPheCysArgLeuThrValLeuLeuLeuValPheGlyPhe 376
QY 1184 AGTTGATGTCACATACACCTTTTCCATGTGTGTAAGTATTTAATGACAACTTATTTCA 1243
Db 377 SerTyrMetProLeuHisLeuPheHisIleValThrAspPheAsnAlaThrLeuLeuSer 396
QY 1244 AATAGGCAATTCAGTTGGTGTATGCTATTCATTCATTTGTTGGCATGATGCTCTGTGT 1303
Db 397 AsnArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetSerCysCys 416
QY 1304 CTTAATCAATTCATATGTTGTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTT 1363
Db 417 LeuAsnProIleLeuTyrGlyPheLeuAsnAsnSerIleLysAlaAspLeuMetSerLeu 436
QY 1364 ATACACTGT 1372
Db 437 IleProCys 439

RESULT 11
ID O73733 PRELIMINARY; PRT; 377 AA.
AC O73733;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Y/peptide YY receptor Ya.
GN Name=NPYr; Synonyms=NPYrA; (Danio rerio).
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98068942; PubMed=9407007;
RA Lundell I., Berglund M.M., Starback P., Salaneck B., Gehlert D.R.,
RA Larhammar D.;
RT "Cloning and characterization of a novel neuropeptide Y receptor
RT subtype in the zebrafish.";
```

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DNA Cell Biol. 16:1357-1363(1997).
[2]
SEQUENCE FROM N.A. PubMed=9434780;
MEDLINE=98096393;
RX Ringvall M., Berglund M.M., Larhammar D.;
RA "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
RT subtype in the zebrafish.";
RT Biochem. Biophys. Res. Commun. 241:749-755(1997).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=99337783;
RA Starback P., Lundell I., Fredriksson R., Berglund M.M., Yan Y.L.,
RA Wraath A., Soderberg C., Postlethwait J.H., Larhammar D.;
RA "Neuropeptide Y receptor subtype with unique properties cloned in the
RT zebrafish: the zY receptor.";
RT Brain Res. Mol. Brain Res. 70:242-252(1999).
DR EMBL; AF037400; AAC41276.1; -.
DR ZFIN; ZDB-GENE-980526-393; npyrya.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000351; NPY1_receptor.
DR InterPro; IPR000611; NPY1_receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01013; NRPEPTIDEYR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G-PROTEIN_RECIP_F1_1; UNKNOWN 1.
DR PROSITE; PS0262; G-PROTEIN_RECIP_F1_2; 1.
KW Neuropeptide; Receptor.
SQ SEQUENCE 377 AA; 42901 MW; 60B62AD9C7BF5D0 CRC64;
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Alignment Scores:
Pred. No.: 2,148-37 Length: 377
Score: 558.00 Matches: 124
Percent Similarity: 44.24% Conservative: 68
Best Local Similarity: 28.57% Mismatches: 136
Query Match: 22.50% Indels: 106
DB: 2 Gaps: 6

US-09-771-956-4 (1-1406) x O73733 (1-377)
QY 74 AACAGACACTTCCACAGAGAAATAACTGCTGCCACTCGGAATTCGATTTCCAGTC 133
Db 16 AsnSerThrLeuThrHisAsnGlnSerAsnSerLeuPheLeuLeuAspValProCys 35
QY 134 TGGATGACTATAAAGACGAGTGTAGATGACTTACAGTATTTTCTGATTGGGCTCTATACA 193
Db 36 Trp-----GlnSerSerThrMetThrLeuThr-----LeuValLeuCysTyrCys 50
QY 194 TTGTGAAGCTTCTTGGCTTTATGGGAATCTACTTATTTAATGGCTCTCATGAAAAAG 253
Db 51 LeuValLeuLeuLeuGlyLeuLeuGlyAsnIleLeuLeuLeuCysIleIleMetHisGln 70
QY 254 CGTAATCAGAAGACTACGGTAAACTTCTTCATAGCAATCTGCCCTTTCTCATATCTTG 313
Db 71 ArgAspProProAsnValThrSerIleLeuIleAlaAsnLeuSerValSerAspIleLeu 90
QY 314 GTTGTGCTGTTTGTGCTCACTTTTCACATGACGCTGCTGCTTGTGATCAGTGGATGTT 373
Db 91 ValSerValPheCysLeuProPheThrValValTyrThrLeuMetAspHisTrpIlePhe 110
QY 374 GGCAAGTTCATGCGCATATATATGCTTTTCTTCAATGTGTGTGCTGTTTGGTTCAACT 433
Db 111 GlyAlaLeuLeuCysArgLeuMetProPheValGlnCysValSerValThrValSerVal 130
QY 434 TTATTTTATATCAATTCGCTTGTCCATGTCAGTATCATATGATATAAACAATCCATATCTAAT 493
Db 131 LeuSerLeuLeuLeuAlaLeuGluArgHisGlnLeuLeuLeuHisProSerGlyTrp 150
```

QY 494 AATTAAACAGCAACCATGGCTACTTCTGTAGACTACTGCTGCAACACTAGGTTTGGCC 553
 Db : : : : :
 151 LysProSerValProGlnAlaValIleAlaValLeuThrValTrpLeuLeuAlaCysVal 170
 QY 554 ATCTGTTCTCCCTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTCA 613
 Db : : : : :
 171 ThrSerLeuProPheLeuAlaPheHisLeuLeuThrSerGluProTyrSerLeuPhePro 190
 QY 614 GCATTGTCAGCAGCAGGATTTATGTTGAGTCATGGCCATCTGATTCATACAGAAATT 673
 Db : : : : :
 191 AlaProLeuSerGlnLeuGlnValCysLeuGluValTrpProSerGlnAspHisLysLeu 210
 QY 674 GCCTTACTATCTCTTATCTGCTAGTTCAGTATATCTGCTGCTAGTCTTCTTCTAGTGA 733
 Db : : : : :
 211 AlaTyrThrSerLeuLeuPheGlnTyrCysCysProLeuLeuMetLeuLeu 230
 QY 734 AGTCATACAAGTGTCTGCAGAAATAGCTGTGGAATGTTCCAAACAAAGAAACAGACTT 793
 Db : : : : :
 231 CystTyrLeuArgIle----- 235
 QY 794 GAAGAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAGAGAGTGGCCCTCAGGTG 853
 Db : : : : :
 235 ----- 235
 QY 854 AAACCTCTGCGCAGCCATAATGAGTTATTCACTTCAATCAAAAACACAGAAAGATAT 913
 Db : : : : :
 236 -----PheLeuArgLeuGlnArgGluArg 244
 QY 914 AGCAAGAGACAGCATGTGTGTTACTGCTCAGAAAGACCTTCTCAAGAGAACCACTCC 973
 Db : : : : :
 245 MetLeuGluArgGlnCys-----SerArgAsnArgGluAspGluHisArg 259
 QY 974 AGAATCTTCCAGAAACTTTGGCTCTGTAAGAGTCAGTCTCTTCATCCAGTAAGTTC 1033
 Db : : : : :
 260 ArgValMet----- 262
 QY 1034 ATACCAGGGTCCCACTTCTGTTGAGATAAAACCTGAAGAAATTCAGATGTTTCATGAA 1093
 Db : : : : :
 262 ----- 262
 QY 1094 TTGAGAGTAAACGCTTCTGTTACAGAAATATAAAGAGATCTCGAAGTGTTCACAGA 1153
 Db : : : : :
 263 -----HisSerLysArgIleAsnValMet 270
 QY 1154 CTGACCATAGTATGATTTAGTATTGCTGTTAGTGGATGCCACTACACCTTTTCCATGTG 1213
 Db : : : : :
 271 LeuAlaThrLeuValAlaAlaPheAlaValCysTrpLeuProLeuAsnAlaPheAsnVal 290
 QY 1214 GTAATCTGATTTAATGACATCTTATTCAATAGGCAATTCAGTTGGTGTGATTCGATT 1273
 Db : : : : :
 291 ValAlaAspCysAspGlnGluValLeuProValCysAsnHisAsnLeuLeuPheSerLeu 310
 QY 1274 TGTCATTTGTCGCGATGCTGCTGTTGCTTAATCCATCTTATATGCGTTCTTAAT 1333
 Db : : : : :
 311 CysHisLeuLeuAlaMetSerThrCysValAsnProIleIleIleIleIleIleIleIle 330
 QY 1334 AATGGGATTAAAGCTGATTTAGTGTCCCTTATA---CACTGT 1372
 Db : : : : :
 331 SerAsnPheArgLysAspValAlaSerValValLeuHisCys 344

RESULT 12

Q6Y6A4 ID Q6Y6A4 PRELIMINARY; PRT; 348 AA.
 AC Q6Y6A4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE NPX receptor Y1 (Fragment).
 OS Squalus acanthias (spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidae;
 OC Squalidae; Squalus.
 CX NCBI_TaxID=7797;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22763539; PubMed=12777532;
 RA Salaneck E., Ardeil D.H., Larson E.T., Lathammar D.;
 RT "Three neuropeptide X receptor genes in the spiny dogfish, *Squalus*
 RT *acanthias*, support en bloc duplications in early vertebrate
 RT evolution."; Mol. Biol. Evol. 20:1271-1280(2003).
 RL Mol. Biol. Evol. 20:1271-1280(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Salaneck E.W., Larson E.T., Ardeil D.H., Lathammar D.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AY177273; AAO62565.1; -.
 DR EMBL; AY177272; AAO62565.1; JOINED.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000351; NPX_receptor.
 DR InterPro; IPR000611; NPX_receptor.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PRINTS; PRO1013; NRPEPTIDEYR.
 DR PRINTS; PRO1012; NRPEPTIDEYR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 348 348
 SQ SEQUENCE 348 AA; 40738 MW; 817D35C53DAFD90F CRC64;

Alignment Scores:

Align. No.: 7 73e-35 Length: 348
 Score: 527.00 Matches: 115
 Percent Similarity: 43.30% Conservative: 79
 Best Local Similarity: 25.67% Mismatches: 122
 Query Match: 21.25% Indels: 132
 DB: 2 Gaps: 7

US-09-771-956-4 (1-1406) x Q6Y6A4 (1-348)

QY 29 TCACAGCAGGACTATATATGATTTAGCTGACGAGTATTATACAGACACTTGGCC 88
 Db : : : : :
 19 SerGluArgAsnPheThrLeuAsp---AsnTyrAspGlnCysTyrSerGlnThrAla--- 36
 QY 89 ACAGAGAATAATACTGCTGCCACTCGGAATTCGTATTTCCAGTCTGGAGTACTATAA 148
 Db : : : : :
 36 ----- 36
 QY 149 AGCAGTGTAGAGACTTACAGATATTTCTGATTTGGCTCTATACATTGTGAAGTCTCTT 208
 Db : : : : :
 37 -----MetIlePheThrLeuAlaLeuIleTyrSerAlaIleIleLeu 51
 QY 209 GCTTTATGGGAATCTACTTATTATTAATGCTCTCATGAAAAGCGTAACAGACT 268
 Db : : : : :
 52 GlyValSerGlyAsnLeuLeuIleThrIleIleMetLysGlnLysGluMetHisAsn 71
 QY 269 ACGTAAATCTCTCATAGGCAATCTGGCTTTTCTGATATCTGTTGGTGTGCTCTTTGC 328
 Db : : : : :
 72 ValThrAsnIleLeuValAsnLeuSerValSerAspLeuLeuIleSerValMetCys 91
 QY 329 TCACCTTTACACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 388
 Db : : : : :
 92 LeuProPheThrLeuValTyrThrPheMetAspHisIleIlePheGlyGluAlaMetCys 111
 QY 389 CATATTATGCTCTTTCTCAATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
 Db : : : : :
 112 LysLeuAsnSerMetIleGlnCysIleSerIleThrValSerIlePheSerLeuValLeu 131
 QY 449 ATTGCCATTGTCAGGTATCATATGATAAATCCATATCTATATTAATTTAATCAAC 508
 Db : : : : :
 132 IleAlaValGluArgHisGlnLeuIleAsnProGlnGlyTrpArgProAsnAsnLys 151
 QY 509 CATGCTACTTCTGTAGTACTGTCTGCGACACTAGGTTTGGCATCTGCTTCCCTCTT 568

Db 152 HisAlaTyrLeuSerIleValThrMetTyrThrLeuAlaLeuLeuThrSerLeuProPhe 171
QY 569 CAGTGTTCACAGTCTGTGGAACTTCAAGAACATTTGGT---TCACATGTCGTGAC 625
Db 172 LeuLeuPheHisAsnLeuThrAspGluGlnPheHisGlyTyrSerThrGluPheAla 191
QY 626 AGCAGTATTATGCTGTGAGTCATGCCATCTGATTCATACAGAAATTCCTTTTACTATC 685
Db 192 GlyLysTyrMetCysLeuGluGlnTyrProSerGluThrGlnArgLeuValTyrThr 211
QY 686 TCTTTATGCTAGTTCAGTATATCTGCGCTTGTAGTTTGTCTTACTGTAAGTACATCAAGT 745
Db 212 CysLeuLeuValMetGlnTyrPheAlaProLeuCysPheIlePheIleCysTyrPheLys 231
QY 746 GTCGTGAGAAGTATAGCTGTGATGTCCTCAACAAAGAAACAGACTTCGAAGAAATGAG 805
Db 232 Ile----- 232
QY 806 ATGATCAACTTAATCTTTCATCCATCAAAAGAGTGGCGCTCAGGTGAACCTCTCTGCG 865
Db 232 ----- 232
QY 866 AGCCATAATGGAGTTATTCAATCATCAAAACACAGAGAAGATATAGCAAGAGACA 925
Db 233 -----TyrIleArgLeuArgArgAsnAsnThrMet----- 243
QY 926 GCATGTGTGTACTGCTGCAGAAAGACCTCTCAAGAGAACCACTCCAGAAATCTTCCA 985
Db 244 -----AspLysMetArgGluGluAsn----- 250
QY 986 GAAAACTTTGGCTCTGTAAGAAGTACAGTCTCTTCATCCAGTAAGTTCATACACGGGGTC 1045
Db 250 ----- 250
QY 1046 CCACATGCTTTGAGATAAABACCTGAAGAAATTCAGATGTTTCATGAATTCAGAGTAA 1105
Db 251 -----LysTyrArgAlaAspGluAsn----- 257
QY 1106 CGTTCCTGTAAGAATAAAGAGATCTCGAAGTGTTTTCACAGACTGACCATCTG 1165
Db 258 -----ArgArgIleAsnIleMetLeuIleSerIle 267
QY 1166 ATATTAGTATTGCTGTAGTGTGATGCCACTACCTTCCATGTTGGTAACATGATTT 1225
Db 268 ValValAlaPheAlaIleCysTyrLeuProLeuAsnIlePheAsnAlaValPheAspTyr 287
QY 1226 AATGACAATCTATTTCAAATAGGCATTTCAAGTTGGTGTATTCATTTGCTTTGTTG 1285
Db 288 AsnTyrGluValIleAsnAsnCysHisAsnLeuValPheSerIleCysHisLeuThr 307
QY 1286 GGCATGATGCTGCTGTTGTTTAAATCCAAATTCATATGCGTTTCTTAAATATGGATTA 1345
Db 308 AlaMetLeuSerThrCysThrAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGln 327
QY 1346 GCTGATTTAGTGTCCCTTATACAC 1369
Db 328 ArgAspLeuArgSerIleLeuHis 335
RESULT 13
AA062565 PRELIMINARY; PRT; 348 AA.
AC AA062565;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NPY receptor v1 (Fragment).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
CX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.

MDLINE=22763539; PubMed=12777532;
RA Salaneck E., Ardell D.H., Larson E.T., Larhammar D.;
RT "Three Neuroptide Y Receptor Genes in the Spiny Dogfish, Squalus
RT acanthias. Support en Bloc Duplications in Early Vertebrate
RL Mol. Biol. Evol. 20:1271-1280 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Salaneck E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY177273; AA062565.1; -
DR EMBL; AY177272; AA062565.1; JOINED.
KW Receptor.
FT NON TER 348 348
SQ SEQUENCE 348 AA; 40738 MW; 817D35C53DAFD90F CRC64;
Alignment Scores:
Pred. No.: 7, 73e-35 Length: 348
Score: 527.00 Matches: 115
Percent Similarity: 43.30% Conservative: 79
Best Local Similarity: 25.67% Mismatches: 122
Query Match: 21.25% Indels: 132
DB: 2 Gaps: 7
US-09-771-956-4 (1-1406) x AA062565 (1-348)
QY 29 TCCAGAGAGAGTACTAATATGATTTAGAGTTCGACGAGTATTATACACAGACACTTCC 88
Db 19 SerGluArgAsnPheThrLeuAsp---AsnTyrAspGlnCysTyrSerGlnThrAla--- 36
QY 89 ACAGAGAATAATACCTGCTGCCACTCGGAATTCGATTTCCAGTCTGGGATCATATAA 148
Db 36 ----- 36
QY 149 AGCAGTGTAGAGTACTACAGTATTTCTGATGGCTCTATACATTTGTAGTCTTCTT 208
Db 37 -----MetIlePheThrLeuAlaLeuIleTyrSerAlaIleIleLeu 51
QY 209 GCGTTTATGGGAATCTACTATTATTAATGCTCTCATGAAAAAGCGTAATCAGAGACT 268
Db 52 GlyValSerGlyAsnLeuLeuIleThrIleMetLysGlnLysGluMethHisAsn 71
QY 269 ACGGTAACCTTCCTCATAGCAATCTGCGCTTTCTGATATCTTGGTGTGCTGTTTGC 328
Db 72 ValThrAsnIleLeuIleValAsnLeuSerValSerAspLeuIleSerValMetCys 91
QY 329 TCACCTTCACACTGACGCTGCTCTGCTGGATCAGTGTGATCTTTGGCAAGTCTATGTC 388
Db 92 LeuProPheThrLeuValTyrThrPheMetAspHisTyrIlePheGlyGluAlaMetCys 111
QY 389 CATATTATGCCCTTTCTTCAATGTGTGTCAGTTTGGTTTCAACTTTAATTTAATATCA 448
Db 112 LysLeuAsnSerMetIleGlnCysIleSerIleThrValSerIlePheSerLeuValLeu 131
QY 449 ATTGCAATGTCAGGTATCATATGATAAACAATCCATATCTAATAATTTACACGAAC 508
Db 132 IleAlaValGluArgHisGlnLeuIleIleAsnProGlnGlyTyrArgProAsnAsnLys 151
QY 509 CATGGCTACTTCTGATAGTACTGCTGGACACTAGGTTTGGCCATCTGTTCTCCCTT 568
Db 152 HisAlaTyrLeuSerIleValThrMetTyrThrLeuAlaLeuLeuThrSerLeuProPhe 171
QY 569 CCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGT---TCACATGTCGTGAC 625
Db 172 LeuLeuPheHisAsnLeuThrAspGluGlnPheHisGlyTyrSerThrGluPheAla 191
QY 626 AGCAGTATTATGCTGTGAGTCCATCTGATTCATACAGAAATTCCTTTTACTATC 685
Db 192 GlyLysTyrMetCysLeuGluGlnTyrProSerGluThrGlnArgLeuValTyrThr 211
QY 686 TCTTTATGCTAGTTCAGTATATCTTCCCTTGTAGTTTGTCTTACTGTAAGTACATCAAGT 745
Db 212 CysLeuLeuValMetGlnTyrPheAlaProLeuCysPheIlePheIleCysTyrPheLys 231
RP SEQUENCE FROM N.A.


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QY 764 TGTGATGTTCCACAAAGAAAACAGACTTGAAGAAAATGAGATGATCAACTTAACCTTT 823
Db 241 AsnGlyMetAlaAspLys-
QY 824 CATCCATCCAAAAGAGTGGCCCTCAGGTGAACCTCTCTGCGAGCCATAATGGAGTTAT 883
Db 246
QY 884 TCATTTCATCAAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTACCTGCT 943
Db 246
QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATATCTTCCAGAAAACCTTGGCTCTGTA 1003
Db 247 -----MetArgGluAsnGluSerArgVal
QY 1004 AGAAGTCAGCTCTCTTCATCCAGTAAAGTTCATACCAGGGGTCCCACTTGCTTTGAGATA 1063
Db 254
QY 1064 AAACCTGAAGAAAATTCAGATGTCATGAATGAGAGTAAGAACCTTCTGTGTACAGAATA 1123
Db 254
QY 1124 AAAAAGAGATCTCGAAGTGTCTTACAGACTGACCATCTGATATTAGTATTGCTGTT 1183
Db 255 ---AsnGluSerLysArgIleAsnMetMetLeuAlaSerIleValAlaPheThrVal
QY 1184 AGTTGGATGGCACTACACCTTTTCCATGTGGTAACTGATTTTAAATGACAATCTTAATTC 1243
Db 274 CysTrpLeuProLeuAsnIlePheAsnValValPheAspTrpAsnHisGluAlaLeuMet 293
QY 1244 AATAGGATTTCAAGTTGGTGTATGTCATTTGTCATTTGTTGGCATGATGCTGTTGT 1303
Db 294 AsnCysHisTrpAsnLeuValPheThrLeuCysHisLeuThrAlaMetIleSerThrCys 313
QY 1304 CTTAATCCAAATTCATATGCTGTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCTTT 1363
Db 314 IleAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnLysAspLeuAsnMetLeu 333
QY 1364 ATACACTGT 1372
Db 334 IleHisCys 336

RESULT 15
AAO62564 PRELIMINARY; PRT; 373 AA.
AC AAO62564;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NPV receptor Y6.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22763539; PubMed=12777532;
RA Salanek E., Ardell D.H., Larson E.T., Larhammar D.;
RT "Three Neuropeptide Y Receptor Genes in the Spiny Dogfish, Squalus
RT acanthias, Support en Bloc Duplications in Early Vertebrate
RT Evolution.";
RL Mol. Biol. Evol. 20:1271-1280 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Salanek E.W., Larson E.T., Ardell D.H., Larhammar D.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY17721; AAO62564.1; -.
KW Receptor.
SQ SEQUENCE 373 AA; 42961 MW; 652E44A1F11DE9F5 CRC64;

Alignment Scores:

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Pred. No.: 1.83e-34 Length: 373
Score: 522.50 Matches: 117
Percent Similarity: 42.44% Conservative: 71
Best Local Similarity: 26.41% Mismatches: 134
Query Match: 21.07% Indels: 121
DB: 2 Gaps: 7

US-09-771-956-4 (1-1406) x AAO62564 (1-373)
QY 71 TATAACAAGACACTGCCACAGAGATAATACTGTGCCACTCGGAATTTCTGATTTCCTCA 130
Db 6 TyrAsnHisSerVal-----AsnIleSerGluValIleHisAspGlyThrArgPro 22
QY 131 GTCCTGGATGACTATAAAGC-----AGTGTAGATGACTTACAGTATTTTCTGATGGG 184
Db 23 GlnPheAlaAspPheAspSerCysGlnAlaSerSerProValMetPheLeuLeuLeuLeu 42
QY 185 CTCATACATTTGTAGTCTTCTGCTTTATGGGAATCTACTTATTATTAATGCTCTC 244
Db 43 AlaTyrGlyThrValThrIleValGlyLeuPheGlyAsnLeuCysLeuIlePheIleIle 62
QY 245 ATGAAAAGCGTAATCAGAAGACTAGCGTAAACTTCTCATAGGCAATCTGGCCTTTTCT 304
Db 63 LysArgGlnLysGluAsnHisAsnValThrAsnIleLeuIleAlaAsnLeuSerValSer 82
QY 305 GATATCTTGGTGTGCTGTTTGTCTCACCCTTTCACACTGACGCTGTCTTGTGTCGATCAG 364
Db 83 AspValPheIleCysValMetCysIleProPheThrIleValTyrThrLeuMetAspTyr 102
QY 365 TGGATGTTTGGCAAGTTCATGTGCCATATTATGCTTTTCTTCAATGTGTGTCAGTTTG 424
Db 103 TrpIlePheGlyAspIleMetCysLysAlaAsnSerPheIleGlnCysValSerValThr 122
QY 425 GTTTCACCTTTAATTTAATATCAATTCGCATGTCCAGTATGTCAGTATCATATGATAAATCC 484
Db 123 ValSerIlePheSerLeuValLeuIleAlaIleGluArgHisGlnLeuIleValAsnPro 142
QY 485 ATATCTAATAATTTAACGCAACCATGGCTACTTCTTCATAGCTACTGTCTGGACACTA 544
Db 143 ArgGlyTrpLysProSerValSerHisAlaCysTrpGlyIleValLeuIleTrpPheVal 162
QY 545 GCTTTTGCATCTGTTCTCCCTTCCAGTGTTCACAGTCTTTGTGGAATTCAGAAACA 604
Db 163 SerLeuIleIleSerPheProPheIleIlePheHisLeuLeuThrAsp-----GluPro 180
QY 605 TTT-----CGTTTCAGATGCTGACGACGACGATTTATTTGCTTTCAGTCA 649
Db 181 PheArgAsnValSerSerHisSerGluPheTyrLysAspLysPheValCysIleGluIle 200
QY 650 TGGCATCTGATTCATACAGAAATTCCTTACTATCTCTTTTATTTAGTTCAGTATATT 709
Db 201 TrpProSerGluAlaAspArgLeuValPheThrThrCysLeuLeuLeuLeuGlnTyrPhe 220
QY 710 CTGCTCTTGTGTTGCTTACTTACTTAAGTATACAAAGT-----GTCTGAGAAAGTATAAGC 763
Db 221 AlaProLeuCysPheIlePheValCysTyrLeuLysIlePheValCysLeuLysLysArg 240
QY 764 TGTGGATTCCTCAACAAAGAAAACAGACTTGAAGAAAATGAGATGATCAACTTAACCTT 823
Db 241 AsnGlyMetAlaAspLys-----
QY 824 CATCCATCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGCGAGCCATAATGGAGTTAT 883
Db 246 -----
QY 884 TCATTTCATCAAAAACACAGAAGAAGATATAGCAAGAAGACAGCATGTGTGTACCTGCT 943
Db 246 -----
QY 944 CCAGAAAGACCTTCTCAAGAGAACCACTCCAGATATCTTCCAGAAAACCTTGGCTCTGTA 1003
Db 247 -----MetArgGluAsnGluSerArgVal-----

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QY 1004 AGAAGTCAGCTCTCTTCATCCAGTAAGTTCATACCAGGGTCCCACTTGTCTTGAGATA 1063
Db 254 ----- 254
QY 1064 AAACCTGAAGAAATTCAGATGTTTCATGAATTGAGAGTAAACCGTTCCTGTTACAGAATA 1123
Db 254 ----- 254
QY 1124 AAAAAGAGATCTCGAAGTGTTTCTACAGACTGACCATAGTATAGTATTGCTGTT 1183
Db 255 ---AsnGluSerLysArgIleAsnMetMetLeuAlaSerIleValValAlaPheThrVal 273
QY 1184 AGTTGGATGCCACTACACCTTTTCCATGCTGTAATGATGATTTAATGACAATCTTATTCA 1243
Db 274 CysTrpLeuProLeuAsnIlePheAsnValValPheAspIrpAsnHisGluAlaLeuMet 293
QY 1244 AATAGGCATTTCAAAGTTGGTGTATTGTCATTTGTTGGGCATGATGTCCTGTTGT 1303
Db 294 AsnCysHisTyrAsnLeuValPheThrLeuCysHisLeuThraAlaMetIleSerThrCys 313
QY 1304 CTTAATCCAATCTATATGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTT 1363
Db 314 IleAsnProIlePheTyrGlyPheLeuAsnLysAsnPheGlnLysAspLeuAsnMetLeu 333
QY 1364 ATACACTGT 1372
Db 334 IleHisCys 336
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Search completed: October 21, 2004, 11:57:50
Job time : 315.5 secs

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15646-4

Alignment Scores:

Pred. No.: 3,786-270 Length: 456
Score: 2386.00 Matches: 456
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.21% Indels: 0
DB: 5 Gaps: 0

US-09-771-956-4 (1-1406) x PCT-US95-15646-4 (1-456)

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QY	77	AAAGACACTTGCACAGAGATATATCTGCTGCACCTCGGAATCTCGATTTCCAGTCTGG	136
Db	21	LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp	40
QY	137	GATGACTATAAAGCAGCTAGATGACTTACAGTATTTCTGATTTGGGCTCTATACATTT	196
Db	41	AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe	60
QY	197	GTAAGTCTTCTGGCTTTATGGGAACTCTACTATTATTTAATGGCTCTCATGAAAAGCGT	256
Db	61	ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg	80
QY	257	AATCAGACACTACGCTAAACTCTCTCATAGCAATCTGGCTTTCTCGATATCTTGTT	316
Db	81	AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal	100
QY	317	GTGCTGTTTGTCTACCTTTTACACAGCTCTGTCTGCTGGATCAGTGGATTTGGC	376
Db	101	ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly	120
QY	377	AAAGTCATGTCATATATGCTTTCTTCAATGTGTGTCAGTTTGGTTTCAACTTA	436
Db	121	LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu	140
QY	437	ATTTTATATCAATGTCAGGTATCATATGATATAAACAATCCATATCTAATAAT	496
Db	141	IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn	160
QY	497	TTAAGACAAACCATGGCTACTTCTGTAGTACTGTCTGGACACTAGGTTTGGCATC	556
Db	161	LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle	180
QY	557	TGTTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTACGA	616
Db	181	CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla	200
QY	617	TGCTGACGACAGATATTTATGTGTGAGTCATGGCCATCTGATTATCATACAGAAATGCC	676
Db	201	LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla	220
QY	677	TTTACTATCTCTTTATCTAGTTACGATATTTCTGCCCCTAGTTTCTTACTGTAAGT	736
Db	221	PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer	240
QY	737	CATCAAGTGTCTCAGAGATATAAGCTGTGGATTTGTCCAAAGAAACACAGCTTGA	796
Db	241	HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu	260
QY	797	GAAATGATGATCACTTAACCTTTCATCCATCCAAAGAGATGGGCTCAGGTGAAA	856
Db	261	GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys	280
QY	857	CTCTCTGACCCCAATGAGGTATTTCATTCATCAAAAAACACAGAAAGATATAGC	916
Db	281	LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer	300

QY	917	AAGAAGACAGCATGTGTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA	976
Db	301	LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg	320
QY	977	ATACTTCCAGAAACTTTGGCTCTGTAAAGAGTCAGCTCTCTTTCATCCAGTAAGTTTATA	1036
Db	321	IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle	340
QY	1037	CCAGGGTCCCACTTGTCTTGAGATTAACACCTCGAAGAAATTCAGATCTTCATGAATG	1096
Db	341	ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu	360
QY	1097	AGAGTAAACGTTCTGTTCACAGAAATAAAAAAGAGATCTCGAAGTGTCTTCTACAGACTG	1156
Db	361	ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu	380
QY	1157	ACCATACTGATATATGATTTGCTGTAGTTGGATCCCACTACACCTTTTCCATGTGTA	1216
Db	381	ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal	400
QY	1217	ACTGATTTTAAATGACAACTCTTATTTCAAATAGGCATTTCAAAGTTGGTGTATTGCATTTGT	1276
Db	401	ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys	420
QY	1277	CATTGTTGGGATGATGCTGTTGCTTTAAATCCAAATCTATATGGGTTTCTTTAATAAT	1336
Db	421	HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn	440
QY	1337	GGGATTAAGCTGATTTAGTTCCTTATACACTGTCTTCATATGTA	1384
Db	441	GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet	456

RESULT 2

US-08-349-025-4
Sequence 4, Application US/08349025
Patent No. 5602024
GENERAL INFORMATION:
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HYPOTHALAMIC ATYPICAL
NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,025
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-349-025-4

Alignment Scores:
Pred. No.: 4,94e-270 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: 1 Gaps: 0

US-09-771-956-4 (1-1406) x US-08-349-025-4 (1-455)

QY	17	ATGTCCTTTTATCCACAGCAGCTATAATATGAGTTAGAGCTCGACGAGTATTATPAAC	76
DB	1	MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn	20
QY	77	AAGACATGTCACAGAGATAAATCTGCTCCCACTCGGAATCTGATTTCCAGCTGG	136
DB	21	LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr	40
QY	137	GATGACTATAAAGCAGTGTAGATGACTTACAGTATTTCTGATTGGCTCTATACATTT	196
DB	41	AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe	60
QY	197	GTAAGTCTCTTGGCTTTATCGGGAATCTACTTATTTAATGGCTCTCATGAAAAGCGT	256
DB	61	ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg	80
QY	257	AATCGAAGACTACGTTAACTTCTCTATAGCAATCTGGCTTTCTGATATCTTGGTT	316
DB	81	AsnGlnTyrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal	100
QY	317	GTGCTGTTTGTCTACCTTTTACACTGACGCTCTGTTCTGTCGATGAGTGGTTCGGC	376
DB	101	ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTyrMetPheGly	120
QY	377	AAAGTCATGTCGCATATATGCTTTCTTCAAGTGTCTCAGTTTGGTTTCAACTTA	436
DB	121	LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu	140
QY	437	ATTTTAAATCAATGGCAATGTGAGGTATCATATGATAAACAATCCCATATCTAATAAT	496
DB	141	IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn	160
QY	497	TTACAGCAAAACCATGGTACTTTCTGATAGTACTGTCTGACACTAGTTTTCGCATC	556
DB	161	LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle	180
QY	557	TGTTCTCCCTTCCAGTCTTTCACAGTCTTGTGGAACTTCAAGAACATTTGGTTTCAGCA	616
DB	181	CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla	200
QY	617	TTGCTGAGCAGCAGGTATTATGCTGTGATGTCATGCCATCTGATTCATACAGAAATGCC	676
DB	201	LeuLeuSerSerArgTyrLeuCysValGluSerTyrProSerAspSerTyrArgIleAla	220
QY	677	TTTACTATCTTTATGCTAGTTCAGTATATCTGCTTGTGCTTGTCTTCTTCTACTAGT	736
DB	221	PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer	240
QY	737	CATACAGTGTCTGAGAAAGTATAAGCTGTGATTGTCCAAACAAAGAAAACAGACTTGA	796
DB	241	HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu	260
QY	797	GAATATGATGATCACTTAATCTTCTTCATCCATCCAAAGAGTGGGCTCAGGTGAAA	856
DB	261	GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys	280
QY	857	CTCTCTGGCAGCATTAATGGAGTATTCTCATCAAAAACACAGAGAGATATAGC	916
DB	281	LeuSerGlySerHisLysIrrpSerTyrSerPheIleLysLysHisArgArgArgTyrSer	300

QY	917	AAGAAGACAGCATGTGTGTACTCTCTCAGAAAGACCTTCTCAAGAGAACACTCCAGA	976
DB	301	LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg	320
QY	977	ATACTTCCAGAAAACCTTTGGCTCTGTAAGAAGTCTGCTCTTTCATCCAGTAAAGTTTATA	1036
DB	321	IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle	340
QY	1037	CCAGGGGTCCCCACTTGTCTTTCAGATAAAACCTGAGAAAATTCAGATGTTTCATGAATG	1096
DB	341	ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu	360
QY	1097	AGAGTAAACGTTCTGTACAGAAATAAAGAGATCTCGAAGTGTTCCTACAGACTG	1156
DB	361	ArgValLysArgSerValThrArgIleLysLysArgSerValPheIleValVal	380
QY	1157	ACCATACTCATATTACTTGTCTGTTAGTTCGATGCCACTACACTTTCATGTTGTTA	1216
DB	381	ThrIleLeuIleLeuValPheAlaValSerTyrMetProLeuHisLeuPheHisValVal	400
QY	1217	ACTGATTTTAAATGACAACTTTATTTCAATAGAGCATTCAGTTCGTTGTTGTTTCT	1276
DB	401	ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys	420
QY	1277	CATTCTTGGCATGATGCTCTGTTCTTAAATCCAATCTATATGGGTTTCTTATAAT	1336
DB	421	HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn	440
QY	1337	GGGATTTAAAGCTGATTTAGTGTCCCTTATACACTGTCTTTCATATG	1391
DB	441	GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet	455

RESULT 3

US-08-566-096A-4
Sequence 4, Application US/08566096A
Patent No. 5968819
GENERAL INFORMATION:
APPLICANT: Getald, Christophe P.G.
APPLICANT: Walker, Mary W.
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: METHODS OF MODIFYING FEEDING BEHAVIOR, DNA ENCODING A HYPOTHALAMIC NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF
TITLE OF INVENTION: COMPOUNDS USEFUL IN SUCH METHODS, AND DNA ENCODING A HYPOTHALAMIC NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR (Y5) AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,096A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/46166-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid

; LENGTH: 455 amino acids

; TYPE: amino acid		
; TOPOLOGY: linear		
; MOLECULE TYPE: protein		
US-08-668-650B-4		
Alignment Scores:		
Pred. No.:	4,946-270	Length: 455
Score:	2385.00	Matches: 455
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	96.17%	Indels: 0
DB:	2	Gaps: 0
US-09-771-956-4 (1-1406) x US-08-668-650B-4 (1-455)		
Qy	17	ATGCTCTTTTATCCAGAGAGACTATAATATGAGTTAGAGCTCGACGAGTATTATAC 76
Db	1	MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
Qy	77	AAGACACTTGGCCAGAGATAATACCTGCTGCCACTCGGAATCTGATTTCCCGAGCTGG 136
Db	21	LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTip 40
Qy	137	GATCACTATAAAGCAGTGTAGTACTTACAGTATTTTCTGATTTGGGCTCTATACATT 196
Db	41	AspAspTyrLysSerSerValAspLeuGlnTyrPheLeuLeuGlyLeuTyrThrPhe 60
Qy	197	GTAAGTCTTCTGCTTTATGGGAATCTACTTATTTTAAATGGCTCTCATGAAAAAGCGT 256
Db	61	ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg 80
Qy	257	AATCAGAGAGACTACGGTAAACTTCTCTCATAGCAATCTGGCCTTTTCTGATATCTGGTT 316
Db	81	AsnGlnLysThrThrValAsnPheLeuLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
Qy	317	GTGCTGTTTCTCACCTTTCACACTGACGCTCTGCTTGTGGATCAGTGGATTTTGGC 376
Db	101	ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
Qy	377	AAAGTCATGTCCCATATTATCCCTTTTCTCAATGTGTGTGTCAGTGTGGTTTCAACCTTA 436
Db	121	LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
Qy	437	ATTTTATATCAATGGCATTTGTCAGGTATCATATGATAAACAATCCCATCTCTAATAAT 496
Db	141	IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
Qy	497	TTACAGCAAAACCATGGCTACTTTCTGATAGCTACTGTCGACACTAGGTTTTCGCCATC 556
Db	161	LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle 180
Qy	557	TGTTCTCCCTTCCAGTGTCTTTCACAGTCTTGTGGAACCTCAAGAAACATTTGGTTCAGCA 616
Db	181	CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
Qy	617	TTGCTGACAGCAGTATTATGTTGTGAGTCAGTGGCCATCTGATTCATACAGAAATGCC 676
Db	201	LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
Qy	677	TTTACTATCTTTTATTGCTAGTTCAGTATATTTGCCCCCTTAGTTTGTCTTACTGTAGT 736
Db	221	PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
Qy	737	CATCAAGTGTCTGAGAGTATAGTGTGGATTTGTCCAAAGAAAGAAACAGACTTGAA 796
Db	241	HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
Qy	797	GAAATGAGATGATCACTTACTTCTTCATCCATCCAAAAAGAGTGGCCCTCAGGTGAAA 856
Db	261	GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
Qy	857	CTCTCTGGCAGCCATAAATGGAGTTATTCAITTCATCAAAAAACAGAGAGATATAGC 916

RESULT 5

```

US-09-200-673-4
; Sequence 4, Application US/09200673A
; Patent No. 6316203
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Walker, Mary W.
; APPLICANT: Branchek, Theresa
; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
; TITLE OF INVENTION: in Such Methods, and DNA Encoding A Hypothalamic
; TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide YY Receptor (Y5)
; FILE REFERENCE: 46166-B2/JPW
; CURRENT APPLICATION NUMBER: US/09/200,673A
; CURRENT FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: 08/566,096
; EARLIER FILING DATE: 1995-12-01
; EARLIER APPLICATION NUMBER: 08/349,025
; EARLIER FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-200-673-4

Alignment Scores:
Pred. No.: 4,946-270 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: 3 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-200-673-4 (1-455)

Qy 17 ATGCTCTTTTATCCAGAGAGACTATAATATGAGTTAGAGCTCGACGAGTATTATAC 76
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101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
377 AAAGTCATGTGCCATATATATGCGCTTTCTTCAATGTGTGTGTCAGTTTGGTTTCAACTTAA 436
121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
437 ATTTTATATCAATGTCATGTCAGTATCATATGATATAAAACATCCCATATCTATATAT 496
141 IleLeuLeuSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsn 160
497 TTAACAGCAAAACCATGCTACTTCTCATAGTACTCTCTGGACACTAGGTTTGGCATC 556
161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
557 TGTTCTCCCTTCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTGGTTAGCA 616
181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200
617 TTGCTGAGCAGCAGTATTTATGTGTGAGTCAATGCGCATCTCATACACAAATGCG 676
201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
677 TTTACTATCTCTTTATGCTAGTTTCAGTATATTTCTGCCCTTAGTTGTCTTACTGAAGT 736
221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
737 CATACAGTCTCTCAGAGATATAGCTGTGGATTGTCCACAAAGAAACACAGACTGAA 796
241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
797 GAAATCAGATGATCAACTTCTTCACTCCATCCAAAAGAGTGGCGCTCAGGTGAAA 856
261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
857 CTCTCTGGCAGCCATAAATGGAGTTTATTCATTCATAAAAAACACAGAAAGATATAGC 916
281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
917 AAGAAGACAGCATGTGTGTACCTGCTCCAGAAAGACCTTCTCAAGAAACCACTCCAGA 976
301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
977 ATACTTCCAGAAAACCTTGGCTGTGTAGAAAGTCAGTCTCTTCATCCAGTAAGTTCA 1036
321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
1037 CCAGGGTCCCACTGCTTTCAGATATAACCTCAAGAAATTCAGATGTTTCATGAATG 1096
341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360
1097 AGAGTAAACCGTCTGTGTACAGAAATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156
361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
1157 ACCATACGTATATAGTATTTGCTGTGTAGTTGGATGCCACTACACCTTTCCATGGTA 1216
381 ThrIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
1217 ACTGATTTAATGACAATCTTATTTCAATAGGCAATTTCAAGTTGGTGTATGTCATTGT 1276
401 ThrAspPheAsnAspAsnLeuLysSerAsnArgHisPheLysLeuValTyrCysIleCys 420
1277 CATTTGTTGGCAGATGCTGTTGCTTAAATCAATTCATATGCGGTTTCTTAATAT 1336
421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsn 440
1337 GGGATTAAGCTGATTTAGTCTCCCTTATACACTGCTTTCATATG 1381
441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 7
US-10-013-846-7

; Sequence 7, Application US/10013846
; Patent No. 6S66367
; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Brielmann, Harry L
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Marlys
; TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
; FILE REFERENCE: 3n-spiroisobenzofuran-1,4'-piperidines
; CURRENT APPLICATION NUMBER: US/10/013,846
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 455
; TYPE: PRT
; ORGANISM: homosapiens
; US-10-013-846-7

Alignment Scores:
Pred. No.: 4,948-270 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
Gaps: 0
DB: 4

US-09-771-956-4 (1-1406) x US-10-013-846-7 (1-455)

QY 17 ATGTCTTTTATTCACAGCAGCACTATAATATGAGTTAGACTCGACAGATATTATAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTrpAsn 20
QY 77 AAGACACTTGCACAGAGATATATCTGCTGCGCACTCGGAATTCGTATTCCTCCAGTCTGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
QY 137 GATGACTATAAAAGCAGCTAGATGACTTACAGTATTTTCTGATTTGGGCTCTATCATTT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAAGTCTTCTGCTTTATGGGGAATCTACTATTTTAAATGCTCTCATGAAAAGCGT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAAGACACTACGGTAAACTTCCTCATAGGCAATCTGGCCCTTTTCTGATATCTTGGTT 316
Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY 317 GTGCTGTTTGTCTACCTTTTCACGTGAGTCTGCTTGTCTGGATCAGTGGATGTTGGC 376
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY 377 AAGTCATCTGCCATATATGCTTTTCTCAATGCTGCTCAGTTTGTGTTTCAACTTTA 436
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY 437 ATTTTAAATATCAATGCTCCATTTGTCAGGTATCATATGATAAAACATCCCATATCTAATA 496
Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsn 160
QY 497 TTAACAGCAAAACCATGCTACTTCTCTGATAGTACTGCTGACACTAGTGTTCCTCATC 556
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180

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157 TGTCTCCCTCCAGTGTTCACAGTCTTGTGGAACCTTCAAGAAACATTTGGTTCAGCA 616
181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200
617 TTGCTGACGACGAGTATTTATGTTGAGTCATGCGCCATCTGATTCATACAGAAATGCC 676
201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
677 TTTACTATCTCTTATCTGCTAGTTCAGTATATCTGCGCTTAGTTTGTCTTACTGTAAGT 736
221 PheThrIleSerLeuLeuValGlnThrIleLeuProLeuValCysLeuThrValSer 240
737 CATACAGTGTCTGAGAAATATAGCTGTGATGTTCCAAAGAAACAGACTTGA 796
241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
797 GAAATGAGATGATCAACTTAACCTTTCATCATCCAAAGAGTGGCGCTCAGGTGAA 856
261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
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1097 AGAGTAAACGCTGTTTACAGAAATAAAAGAGTCTCGAAGTGTCTTACAGACTG 1156
361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
1157 ACCATPACTGATATAGTATTTGCTGTAGTTGAGTGCACCTACACCTTTCCAGTGGTA 1216
381 ThrIleLeuLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
1217 ACTGATTTATGATCAATCTTATTCATAGGATTCAGTGTGGTGTATTCGATTTGT 1276
401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
1277 CATTTGTTGGGCGATGATCTCTGTTGTTTAAATCCAATTCATATGGGTTTCTTAATAAT 1336
421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGCTCTCTATATG 1381
441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

```

RESULT 8

```

US-09-447-907-4
; Sequence 4, Application US/09447907
; Patent No. 6645774
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Weinschank, Richard L.
; APPLICANT: Walker, Mary W
; APPLICANT: Branchek, Theresa
; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful in Such M
; FILE REFERENCE: 1795-46166CA
; CURRENT APPLICATION NUMBER: US/09/447,907
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 08/668,650
; PRIOR FILING DATE: 1996-06-04

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Y5 cdna clone
US-09-447-907-4

Alignment Scores:
Pred. No.: 4 94e-270 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: Gaps: 0

US-09-771-956-4 (1-1406) x US-09-447-907-4 (1-455)

QY 17 ATGCTCTTTTATTCOAAGCAGACTATATATATGATTTAGAGCTCGACAGTATTATTAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
QY 77 AAGACACTTGCACAGAGATAATACTGCTGCCTCGAATTCCTGATTTCCAGTCTGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
QY 137 GATGACTATAAAGCAGGTGTAGACTTACAGTATTTTCTGATTGGCTCTATACATTT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAACTCTTCTGGCTTATGGGAATCTACTATTATTTAAATGGCTCTCATGAAAAGCGT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAGAACACTACGTAACCTTCCTCATAGGCAATCTGGCTTTTCTGATATCTTGTT 316
Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY 317 GTGCTGTTTGTCTACCTTTACACTGAGCTGTCTGCTGGATCAGTACGATGTTGCG 376
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY 377 AAAGTCATGTGCGCATATTATGCTTTTCTCAATGTGTGTGCTGAGTGTTCGTTTCAACTTTA 436
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY 437 ATTTAATATCAATTTGCCATTTGCTAGGTATCATATGATAAAACATCCCATATCTAATAAT 496
Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
QY 497 TTAACAGCAAAACATGGCTACTTTCTGATAGTACTGTCTGACACTAGGTTTTCGCATC 556
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
QY 557 TGTCTTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTTCAGAAACATTTGGTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGlnThrPheGlySerAla 200
QY 617 TTGCTGACGACGAGTATTTATGTTGAGTCAATGCGCCATCTGATTCATACAGAAATGCC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY 677 TTTACTATCTCTTATTTGCTAGTTCAGTATATCTGCGCTTAGTTTGTCTTACTGTAAGT 736
Db 221 PheThrIleSerLeuLeuValGlnThrIleLeuProLeuValCysLeuThrValSer 240
QY 737 CATACAGTGTCTGAGAAATATAGCTGTGATGTTCCAAAGAAACAGACTTGA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
QY 797 GAAATGAGATGATCAACTTAACCTTTCATCATCCAAAGAGTGGCGCTCAGGTGAA 856

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Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
Qy 857 CTCTCTGGCCACCAATAGAGTATTATCATCAAAACACAGAAAGATATAGC 916
Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
Qy 917 AAGAAGACAGCATGTGTGTACCTGCCAGAAAGACCTTCTCAAGAGAACCACTCCAGA 976
Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
Qy 977 ATACTCCAGAAACTTGGCTCTGTAAGAAGTCAGCTCTCTCATCCAGTAAGTTCATA 1036
Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
Qy 1037 CCAGGGTCCCACTGCTGTGTAGATATAAACCCTCAAGAAATTCAGATGTTTCATGAATG 1096
Db 341 ProGlyValProThrCysPheGluIleLysProGluAsnSerAspValHisGluLeu 360
Qy 1097 AGACTAAACGCTTCTGTACAGAAATAAAGAGATCTCGAAGTGTCTTCTCAGACTG 1156
Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
Qy 1157 ACCACTAGTATTAGTATTGCTGTAGTTGGATGCCACTACACCTTTTCCATGCGTA 1216
Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
Qy 1217 ACTGATTTTAATGACATCTTATTCAATAGGCAATTCAGTGTGTATTCGATTGT 1276
Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
Qy 1277 CATTTGTTGGCAGTATGCTCTGTGTCTTAATCCAAATTCATATGCGTTTCTTAATAAT 1336
Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
Qy 1337 GGGATTAAGCTGATTAGTGTCTCTTATACATGCTTCTCATATG 1381
Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 9
US-08-630-118A-6
; Sequence 6, Application US/08630118A
; Patent No. 5919901
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCaleb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; TITLE OF INVENTION: Sequences
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,118A
; FILING DATE: April 8, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149/WH 405
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-118A-6
Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 2 Gaps: 0
US-09-771-956-4 (1-1406) x US-08-630-118A-6 (1-445)
Qy 47 ATGGATTATAGACTCGACGAGTATTATAACAGACACTTCCACAGAGATAATACTGCT 106
Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
Qy 107 GCACCTCGGAATTTCTGATTTCCAGTCTGGGATGACTATAAAAGCAGTGTCAGACTTA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
Qy 167 CAGTATTTCTGATGGGCTCTATACATTTGAAGTCTTCTTGGCTTTATGGGGAATCTA 226
Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
Qy 227 CTTATTTTAAATGGCTCTCATGAAAAGCGTAATCAGAGACTACGTAACCTTCCTCATA 286
Db 61 LeuIleLeuMetAlaLeuMetLysArgAsnGlnLysThrValAsnPheLeuIle 80
Qy 287 GGCATCTGCGCTTTTCTGATATCTTGGTTGTGCTGTTTGTCTCACCTTTCACACTGAG 346
Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
Qy 347 TCTGCTTCTGCTGGATCAGTGGATGTTGGCAAGTCATGTCATATTTATGCTTTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
Qy 407 CAATGTGTGTCAGTTTGGTTTCACTTTAAATTTAAATATCAATTTGCCATTTGTCAGGTAT 466
Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
Qy 467 CATATCATAAACATCCCATATCTAATAATTTAAACAGCAAAACCATGGCTACTTTCTGATA 526
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
Qy 527 GCTACTGTCTGGACACTAGTGTTCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
Qy 587 GTGGAACCTTCAAGAAACATTTGGTTCAGCATTTGCTCAGCAGCAGGATTTATGTGTGAG 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
Qy 647 TCATGGCCATCTGATTCATACAGAAATGGCTTTTACTATCTTCTTATTTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
Qy 707 ATTCTGCCCTTACTGTTGCTTACTGTAAGTCATACAAAGTGTCTGCAAGAGTATAAAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
Qy 767 GGATTGTCCAAACAAAGAAACACAGACTTGAAGAAATGAGATGATCAACTTAATCTTCTAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
Qy 827 CCATCCAAAAGAGTGGCGCTCAGGTGAAACTCTCTGGCAGGCCATATAATGGAGTTATTCA 886

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Db 261 ProSerLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTySer 280
QY 887 TTCATCAAAAAACAGAGAGATATAGCAAGAGACAGCATGTGTTCACCTGCCA 946
Db 281 PheIleLysHisArgArgTrpSerLysLysThrAlaCysValLeuProAlaPro 300
QY 947 GAAGACCTTCTCAGAGACACCTCCAGATCTCCAGATCTCCAGAAACTTGGCTCTGAAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgLysLeuValLysArgLysValArg 320
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTGTGTTGAGATAAAA 1066
Db 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluLeuLys 340
QY 1067 CCTGAAGAAATTCAGATGTTTCATGAATGAGATGAAGATGTTTCTGTTACAGATAAAA 1126
Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgLys 360
QY 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATAGTATTTGCTGTAGT 1186
Db 361 LysArgSerArgSerValPheTyArgLeuThrIleLeuValPheAlaValSer 380
QY 1187 TGGATGCCACTACACTTTTCCATGCTGTAATGATGATTAATGACAACTTTATTTCAAT 1246
Db 381 TrpMetProLeuHisLeuPheHisValThrAspPheAsnAspAsnLeuLeuSerAsn 400
QY 1247 AGGCATTTCAAGTGTGTTGATGCTATTTGCTATTTGTTGGCATGATGCTGTTGCTT 1306
Db 401 ArgHisPheLysLeuValTyCysIleCysHisLeuLeuGlyMetMetSerCysLeu 420
QY 1307 AATCAATTTCTATATGGTCTTTCTTAATATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366
Db 421 AsnProIleLeuTyArgPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuLeu 440
QY 1367 CACTGCTCTCATATG 1381
Db 441 HisCysLeuHisMet 445

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RESULT 10

US-08-838-399-6
 ; Sequence 6, Application US/08838399
 ; Patent No. 5965392

GENERAL INFORMATION:

APPLICANT: Hu Ph.D., Yinghe
 APPLICANT: McCaleb Ph.D., Michael L.
 APPLICANT: Bloomquist Ph.D., Brian T.
 APPLICANT: Flores-Riveros Ph.D., Jaime R.
 APPLICANT: Cornfield Ph.D., Linda J.
 TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boenhen Fulbert & Berghoff
 STREET: 300 South Wacker Drive
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,399
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Greenfield Ph.D., Michael S.
 REGISTRATION NUMBER: 37,147
 REFERENCE/DOCKET NUMBER: 96,149/WH 405
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 715-1000
 TELEFAX: (312) 715-1234
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 445 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-838-399-6

Alignment Scores:

Pred. No.: 1,34e-263 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 2 Gaps: 0

US-09-771-956-4 (1-1406) x US-08-838-399-6 (1-445)

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QY 107 GCACCTCGGAATCTGATTTCCAGTCTGGGATGACTATAAAGCAGGTAGATGACTTA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
QY 167 CAGTATTTCTGATGGGCTCTATACANTTGTAACTCTTCTGGCTTTATGGGAATCTA 226
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QY 227 CTTATTTTAATGGCTCTCATGAAAAGCGCTAATCAGAGACTACGGTAAACTTCCTCATA 286
Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuLeu 80
QY 287 GGCATCTGGCCTTTCTGATATCTTGGTGTGCTGTTTGGCTCCTCACCCTTCACATGAG 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValLeuValPheCysSerProPheThrLeuThr 100
QY 347 TCTGTCTTCTGCTGATCAGTGGATGTTTGGCAAAGTCATGTCCATATTATGCTTTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
QY 407 CAATGTGTGTCAGTTTGGTTTCAACTTAATTTTAATATCAATGCCATGTCAGGTAT 466
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QY 467 CATATGATAAAACATCCCATATCTAATAATTTAACAGCAACCATGGCTACTTTCTGATA 526
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QY 527 GCTACTGTCTGCACACTAGTTTTCCTCATCTGTTTCCCTTCCCTTCCAGTGTTCACAGT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
QY 587 GTGGAACTCAAGAAACATTTGGTTTTCAGCATGCTGACGACGAGGATTTATGTTGAG 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
QY 647 TCATGGCCATCTGATTCATACAGAAATTCCTTTTACTATCTCTTTTATTTCTAGTTCAGT 706
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QY 707 ATTCGCTTGTAGTTTGTCTTACTGTAAGTCATACAGTGTCTGAGAGATATAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrValCysArgSerIleSerCys 240
QY 767 GGATTTGTCCAAACAAAGAAACAGACTTCGAAGAAATGAGATGATCAACTTAACTTTCAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
QY 827 CCATCCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGCGACGCCATAAATGAGATTATTCA 886

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Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
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Qy 947 GAAAGACCTTCTCAAGAGAACCTCCAGATACTCCAGAAAACCTTTGGCTCTGTAAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgLleLeuProGluAnPheGlySerValArg 320
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Db 401 ArgHisPheLysLeuValTyrCysileCysHisLeuLeuGlyMetMetSerCysLeu 420
Qy 1307 AATCCAAATTCATATGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTGCCCTTATA 1366
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Qy 1367 CACTGTCTTCATAG 1381
Db 441 HisCysLeuHisMet 445

RESULT 11
US-09-003-199-21
; Sequence 21, Application US/09003199
; Patent No. 5985616
; GENERAL INFORMATION:
; APPLICANT: Parker, Eric M
; APPLICANT: Strader, Catherine D
; APPLICANT: Rudinski, Mark S
; TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: NJ
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,199
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thampoe, Immac J.
; REGISTRATION NUMBER: 36,322
; REFERENCE/DOCKET NUMBER: CN0775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)298-5061
; TELEFAX: (908)298-5388
; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-003-199-21
Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 2 Caps: 0
US-09-771-956-4 (1-1406) x US-09-003-199-21 (1-445)
Qy 47 ATGGATTTAGAGCTCGACGAGTATTATACAGACACATTCGCCACAGAGNATAATCTGCT 106
Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
Qy 107 GCCACTCGGAATTTCTGATTTCCAGTCTGGGATGACTATAAAAGCAGTGTAGTACACTTA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
Qy 167 CAGTATTTTCTGATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226
Db 41 GlnTyrPheLeuileGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
Qy 227 CTTATTTTAAATGGCTCTCATGAAAAGCGTAATCAGAAGACTACGTAACCTTCCTCAT 286
Db 61 LeuileLeuMetAlaLeuMetLysArgAsnGlnLysThrValAsnPheLeuile 80
Qy 287 GGCAATCTGGCCCTTTTCTGATATCTTGGTTGTGCTGTTTTGTCTACCTTTACACTGACG 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValLeuValPheCysSerProPheThrLeuThr 100
Qy 347 TCTGCTTCTGGATCAGTGGATGTTTGGCAAGTCAATGTCATATTTATGCTTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisileMetProPheLeu 120
Qy 407 CAATGTGTCTGAGTTTGGTTTCACTTTAAATTTTAAATTCATTAATTCAGTATTCAGGTAT 466
Db 121 GlnCysValSerValLeuValSerThrLeuileLeuileSerileAlaileValArgTyr 140
Qy 467 CATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACATGGCTACTTTCTGATA 526
Db 141 HisMetileLysHisProileSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuile 160
Qy 527 GCTACTGTCTGGACACTAGTGTGTCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaileCysSerProLeuProValPheHisSerLeu 180
Qy 587 GTGGAACTTCAAGAAACATTTGGTTTCAGCATTTGTCGAGCAGGATTTATGTGTGAG 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
Qy 647 TCATGGCCATCTGATTCATACAGAAATGGCTTTACTATCTCTTTATTTAGTTCAGTAT 706
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Qy 767 GGATTTCCAAACAAAGAAACAGACTTGAAGAAATGAGATGATGATCACTTAACCTTCAT 826
Db 241 GlyLeuSerAsnLysGluAnArgLeuGluGluAsnGluMetileAsnLeuThrLeuHis 260
Qy 827 CCATCCAAAAAGAGTGGGCTCAGGTGAAACTCTCTGGCAGGCATAAATGGAGTTATTCA 886
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QY 887 TTTCATCAAAAACACAGAGAGATATAGCAAGAGACAGCATGTGTACTCTGCTCCA 946
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QY 947 GAAGACCTTCTCAAGAGAACCTCCAGATATCTCCAGAAAACCTTGGCTCTGTAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTGTCTTGAGATAAA 1066
Db 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
QY 1067 COTGAAGAAAATTCAGATGTTTCATGAATGAGAGTAAACAGCTTCTGTTCACAGAAATAAA 1126
Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
QY 1127 AAGAGATCTCGAAGTGTTTCTACAGACTGACCATGATATAGTATTTGCTGTAGT 1186
Db 361 LysArgSerArgSerValPheTyArgLeuThrIleLeuValPheAlaValSer 380
QY 1187 TGGATGCCACTACACCTTTTCCATGCTGTAATGATGATTTAATGACAATCTTATTTCAAAT 1246
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QY 1247 AGGCATTTCAAGTGGTGTATGCAATTTGTCATTTGTTGGCATGATGCTCTGTGCTT 1306
Db 401 ArgHisPheLysLeuValTyCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420
QY 1307 AATCCAATCTATATGGCTTTCTTAAATGATGAGTAAAGCTGATTTAGTGTCCCTTATA 1366
Db 421 AsnProIleLeuTyGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440
QY 1367 CACTGTCTTCATATG 1381
Db 441 HisCysLeuHisMet 445

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RESULT 12

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US-09-235-839-6
; Sequence 6, Application US/09235839
; Patent No. 6207799
; GENERAL INFORMATION:
; APPLICANT: Hu Ph.D., Yinghe
; APPLICANT: McCaleb Ph.D., Michael L.
; APPLICANT: Bloomquist Ph.D., Brian T.
; APPLICANT: Flores-Riveros Ph.D., Jaime R.
; APPLICANT: Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,839
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,118
; FILING DATE: April 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield Ph.D., Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 96,149-C
; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-235-839-6
Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 3 Gaps: 0
US-09-771-956-4 (1-1406) x US-09-235-839-6 (1-445)
QY 47 ATGGATTATAGAGCTCGACGAGTATTATAACAGACACTTGCACAGAGATAATACTGCT 106
Db 1 MetAspLeuGluLeuAspGluTyTrpAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
QY 107 GCACCTCGGAATTCGATTTCCAGTCTGGGATGACTATAAAGCAGTGTAGATCACTTA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyTrpLysSerSerValAspAspLeu 40
QY 167 CAGTATTTTCTGATGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGCGGAATCTA 226
Db 41 GlnTyPheLeuIleGlyLeuTyTrpPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
QY 227 CTTATTTAATGGCTCTCANGAAAAGCGTAAATCAAGACACTACGGTAAACTTCTCTATA 286
Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80
QY 287 GGCAATCTGGCTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTTCACACTGACG 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValValLeuPheCysSerProPheThrLeuThr 100
QY 347 TCTGTCTTCTGGATCAGTGGATGTTTGGCAAAGTCATGTGCCATATTATGCTTTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
QY 407 CAATGTGTCTGATTTTGGTTTCACTTTAATTAATCAATTCATTCAGTGTAGTAT 466
Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTy 140
QY 467 CATATGATAAAACATCCCATATCTAATAATTTAAACAGCAAAACCTGGTACTTTCTGATA 526
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyPheLeuIle 160
QY 527 GCTACTGTCTGGACACTAGTGTTCGCAATCTGTTCTCCCTTCCAGTGTTCACAGTCTT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
QY 587 GTGGAACTTCAAGAAACATTTGGTTTCAGCATTCGTCAGCAGCAGGTATTTATGTTTGA 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyTrpLeuCysValGlu 200
QY 647 TCATGGCCATCTGATCATACAGAAATTCGCTTTACTATCTCTCTTTATGCTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerTyArgIleAlaPheThrIleSerLeuLeuValGlnTy 220
QY 707 ATTCTGCCCTTAGTTTGTCTTACTGTAAGTCTACAGTGTCTGAGAGATATAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
QY 767 GGATTGTCCACAAAAGAAACAGACTTGAAGAAAATGATGATCACTTAACCTTTTCAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
QY 827 CCATCCAAAAGAGTGGGCTTCAGTGTAACACTCTCTGCGCAGCCATAAATGGAGTTATTCA 886

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Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTySer 280
Qy 887 TTATCAAAAAACACAGAAGAAGATATAGCAAGAGACAGCATGTGTACTGCTCCCA 946
Db 281 PheileLysLysHisArgArgTySerLysLysThrAlaCysValLeuProAlaPro 300
Qy 947 GAAGACCTTCTCAAGAGNACCACTCCAGATATCTCCAGAAACTTTGGCTGTGAAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgLysLeuProGluAsnPheGlySerValArg 320
Qy 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACACAGGGTCCCCACTTCTGTGAGATAAAA 1066
Db 321 SerGlnLeuSerSerSerLysPheLysPheLysProGlyValProThrCysPheGluLeuLys 340
Qy 1067 CCTGAAGAAATTCAGATGTCATGAATTCAGAGTAAACGTTCTGTACAGNATAAAA 1126
Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgileLys 360
Qy 1127 AAGAGATCTCAAGTGTCTTCTACAGACTGACCATCTATGATATAGTATTGCTGTGTAGT 1186
Db 361 LysArgSerArgSerValPheTyArgLeuThrileLeuileLeuValPheAlaValSer 380
Qy 1187 TGGATGCCACTACACCTTTTCATGTGGTAATCTGATTTTAAAGCAATCTTATTTCAAT 1246
Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuileSerAsn 400
Qy 1247 AGGCATTTCAAGTTGGTGATTTGTCATTTGTTGGTCATGATGCTGCTGTGTCTT 1306
Db 401 ArgHisPheLysLeuValTyCysileCysHisLeuLeuGlyMetMetSerCysCysLeu 420
Qy 1307 AATCCAAATTCATATGGTCTTTCTTAATAATGGGATTAAGCTGATTTAGTGTCCCTTATA 1366
Db 421 AsnProLleLeuTyGlyPheLeuAsnAsnGlyileLysAlaAspLeuValSerLeuile 440
Qy 1367 CACTGTCTTCATATG 1381
Db 441 HisCysLeuHisMet 445

RESULT 13
US-09-327-035-6
Sequence 6, Application US/09327035
Patent No. 636824
GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
McCaleb Ph.D., Michael L.
Bloomquist Ph.D., Brian T.
Flores-Riveros Ph.D., Jaime R.
Cornfield Ph.D., Linda J.
TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/327,035
FILING DATE: 07-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,399
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield Ph.D., Michael S.

REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 96,149/WH 405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-327-035-6
Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 230.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 3 Gaps: 0
US-09-771-956-4 (1-1406) x US-09-327-035-6 (1-445)
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Qy 107 GCCACTCGGAATTCGATTTCCAGTCTGGGATGACTATAAAGCAGCTAGTACACTTA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyTyLysSerSerValAspAspLeu 40
Qy 167 CAGTATTTCTGATGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTTA 226
Db 41 GlnTyPheLeuileGlyLeuTyThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
Qy 227 CTTATTTTAAATGGCTCTCATGAAGAAGCGTAATCAAGAGACTACGGTAACCTTCCTCAT 286
Db 61 LeuileLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuile 80
Qy 287 GGCAATCTGGCCTTTTCTCATATCTTGGTGTGCTGTTTTTGTCTACCTTTTCACACTGAG 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValValLeuPheCysSerProPheThrLeuThr 100
Qy 347 TCTGCTTCTGATCAGTGGATGTTGGCAAGTCATGTCATATTAATGCTTTTCTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisileMetProPheLeu 120
Qy 407 CAATGTGTGCTAGTGTGTTTCACTTTTAAATTTTAAATCAATTCATTCATTCAGGTAT 466
Db 121 GlnCysValSerValLeuValSerThrLeuileLeuileSerileAlaileValArgTy 140
Qy 467 CATATGATAAAACATCCCATATCTATAATTTTAAACAGCAAAACATGGCTACTTTCTGATA 526
Db 141 HisMetileLysHisProLleSerAsnAsnLeuThrAlaAsnHisGlyTyPheLeuile 160
Qy 527 GCTACTGTCTGGACACTAGTGTTCATCTGTTTCCCTTCCCTTCCAGTGTTCACAGTCTT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaileCysSerProLeuProValPheHisSerLeu 180
Qy 587 GTGGAACCTTCAAGAAACATTTGTTTCCAGCATTCCTGAGCAGCAGGTATTATTGTGTGAG 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyTyLeuCysValGlu 200
Qy 647 TCATGGCCATCTGATTCATACAGATTGCTTACTATCTTACTTATTGCTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerTyArgileAlaPheThrileSerLeuLeuValGlnTy 220
Qy 707 ATTCTGCCCTTACTTGTCTTACTGTAAGTTCATACAAAGTCTGCAAGAGTATAAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerileSerCys 240
Qy 767 GGATTGTCCAACAAGAAAAACAGACTTGAAGAAATGAGATGATCAACTTAATCTTCTTAT 826

Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
 QY 827 CCATCCAAAAGAGTGGCGCTCAGGTGAACTCTCTGGCAGCCATAAATGGAGTTATCA 886
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysLysTrpSerLysSer 280
 QY 887 TTCATCAAAAACACAGAGAAGATATAGCAAGAAGACAGCATGTGTCTTACCTGCTCCA 946
 Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
 QY 947 GAAAGACCTTCTCAAGAGAACACCTCCAGATATCTCCAGAAAACCTTGGCTGTGAAGA 1006
 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
 QY 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACAGGGGTCCTCCACTTGTGTTGAGATAAAA 1066
 Db 321 SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
 QY 1067 COTGAAGAAAATTCAGATGTTTCATGAATTCAGAGTAAACCTTCTGTTCACAGATAAAA 1126
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
 QY 1127 RAGAGATCTCGAAGTCTTCTTACAGAGTACCATCTGATATAGTATGCTGTAGT 1186
 Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuValPheAlaValSer 380
 QY 1187 TGGATGCCACTACACCTTTTCCATGCTGTAATCTGTAATTAATCAATCTTATTTCAAAT 1246
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400
 QY 1247 AGGCATTTCAAGTGGTGTATGCAATTTGTCATTTTGGGCATGATGCTGTGTCTT 1306
 Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420
 QY 1307 AATCCAATTTCTATATGGTCTTCTTAATTAATGGATTAAGCTGATGCTGCTTATA 1366
 Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440
 QY 1367 CACTGCTTCATATG 1381
 Db 441 HisCysLeuHisMet 445

RESULT 14
 US-09-065-027-2
 ; Sequence 2, Application US/09065027
 ; Patent No. 6528303
 ; GENERAL INFORMATION:
 ; APPLICANT: Herzog, H.
 ; TITLE OF INVENTION: NEUROPEPTIDE Y-Y5 RECEPTOR
 ; FILE REFERENCE: 273402001800
 ; CURRENT APPLICATION NUMBER: US/09/065,027
 ; CURRENT FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: PCT/AU96/00706
 ; PRIOR FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-065-027-2

Alignment Scores:
 Pred. No.: 1,34e-263 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 4 Gaps: 0

US-09-771-956-4 (1-1406) X US-09-065-027-2 (1-445)

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 QY 107 GCCACTCGGAATCTGATTTCCAGCTCTGGGATGACTATAAAGCAGTGTAGATCACTA 166
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
 QY 167 CAGTATTTCTGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 QY 227 CTTATTTTAAATGGCTCTCATGAAAAGCGTAATACAGACACTACCGTAAACTTCCTCAT 286
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle 80
 QY 287 GGCMACTCTGCCTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTACACTGACG 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGTCTTCTGCATCAGTGGATGTTTGGCAAGTCATGTGCCATATATATGCTTTCTT 406
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 QY 467 CATATGATAAAACATCCCATATCTAATTAATTTAAACAGCAAAACCATGGTACTTTCTGATA 526
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
 QY 527 GCTACTGTCTGACACTAGTGTGTCATCTTCTTCCCTTCCAGTGTGTTCACAGTCTT 586
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
 QY 587 GTGGAACCTTCAAGAACATTTGCTTTCAGCATGCTGAGCAGCAGGTATTTATGCTTTCAG 646
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
 QY 647 TCATGGCCATCTGATTCATACAGATTCCTTTTACTTCTTCTTTTATGCTAGTTCAGTAT 706
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 QY 707 ATTCGCTCCCTTGTGCTTACTTACTAGTCTACAGTGTCTGAGAGATATAAGCTGT 766
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
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 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
 QY 827 CCATCCAAAAGAGTGGCGCTCAGGTGAACTCTCTGGCAGCCATAAATGGAGTTATCA 886
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 QY 887 TTCATCAAAAACACAGAGAAGATATAGCAAGAAGACAGCATGTGTGTTTACCTGCTCCA 946
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 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
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Qy 1187 TGGATGCCACATACACCTTTCCATGTGGTAAGTATTTAAATGACAAATCTATTTCMAAT 1246
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Qy 1247 AGGCATTTCAAGTTGGTGTATTGATTTGTCATTGTTGGTCATGATGCTCTGTGTCTT 1306
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Qy 1367 CACTGTCTTCATATG 1381
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RESULT 15
US-09-708-392-13
; Sequence 13, Application US/09708392
; Patent No. 6734186
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; APPLICANT: Pfizer Limited
; APPLICANT: Wayman, Chris
; APPLICANT: Maw, G
; TITLE OF INVENTION: Pharmaceutical
; FILE REFERENCE: PC10343AKW
; CURRENT APPLICATION NUMBER: US/09708,392
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/221,093
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-708-392-13

Alignment Scores:
Pred. No.: 1,34e-263 Length: 445
Score: 2330.00 Matches: 445
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.95% Indels: 0
DB: 4 Gaps: 0
US-09-771-956-4 (1-1406) x US-09-708-392-13 (1-445)
Qy 47 ATGATTTAGCTCGACGAGTATTATTAACAGACACTTGCACAGAGATATATCTGCT 106
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Qy 107 GCACCTCGGAATTCCTGATTTCCAGTCTGGGATGACTATAAAGCAGTGTAGTACTTGA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspAspLeu 40
Qy 167 CAGTATTTTCTGATTTGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTA 226
Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
Qy 227 CTTATTTTAAATGGCTCTCATGAAAGCGTAAATACAGACACTACGGTAAACCTCTCAT 286
Db 61 LeuLeuLeuMetAlaLeuMetLysArgAsnGlnLysThrValAsnPheLeuLeu 80
Qy 287 GGCATCTCGCTCTTTCTCATATCTTGGTGTGCTGTTTGTCTCACCTTTACACTGAGC 346
Db 81 GlyAsnLeuAlaPheSerAspLeuValValLeuPheCysSerProPheThrLeuThr 100
Qy 347 TCTGTCTCTCGATCAGTGGATGTTTGGCAAGCATGTGCCATATATATGCTTTCTTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
Qy 407 CAATGTGTCTCAGTTTGGTTTCACTTTAAATTTAAATCAATTCACATTCACAGTAT 466
Db 121 GlnCysValSerValLeuValSerThrLeuLeuLeuSerIleAlaIleValArgTyr 140
Qy 467 CATATGATAAAACATCCCATATCTAATATTAATTAACAGCAAAACCATGGCTACTTCTG 526
Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu 160
Qy 527 GCTACTGTCTGGACACTAGGTTTGCCTCTCTCTCCCTTCCAGTGTTCACAGTCTT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
Qy 587 GTGGAACTTCAAGAAACATTTGGTTTCAAGTCTGTCAGCAGCAGGATTTATGTGTGAG 646
Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
Qy 647 TCAATGCCATCTGATTCATACAGATTCGCTTACTATCTCTTATTGCTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuLeuValGlnTyr 220
Qy 707 ATTCTGCCCTTAGTTTGTCTTACTGTAACTCATACAAGTGTCTGCAGAGATATAAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
Qy 767 GATTTGCCAACAAAGAAACAGCTTGAAGAAATGAGATGATCACTTACTCTTCTAT 826
Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
Qy 827 CCATCCAAAAGAGTGGGCTCAGGTGAACCTCTCTGCAGCCATAAATGGAGTTATTCA 886
Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
Qy 887 TTCATCAAAAAACACAGAGAAGATATAGCAAGACAGACATGTGTGTTACCTGCTCCA 946
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Qy 947 GAAAGACCTTCTCAAGAGAACCACTCCAGATTAATCTCCAGAAACTTTTGGCTCTGTAAGA 1006
Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
Qy 1007 AGTCAGCTCTTTCATCCAGTAAGTTTCATACAGAGGGTCCCACTTGTCTTTCAGATAAAA 1066
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Qy 1067 CTGGAAGAAAATTCAGATGTTTCAATTAATGAGAGTAAACGGTCTGTTACAGAAATAAAA 1126
Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
Qy 1127 AAGAGATCTCGAAGTCTTTTCTACAGACTGACCATCTCATATTAGTATTTCTGTTAGT 1186
Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuLeuValPheAlaValSer 380

QY	1187	TGGATGCCACTACACCTTTTCCTGCTGTAACCTGATTTTAATGACAATCTTATTCAAAT	1246
Db	381	TrpMetProLeuHisLeuPheHisValThrAspPheAsnAspAsnLeuLeuSerAsn	400
QY	1247	AGGCATTTCAAGTTGGTGATATTCATTTGTCATTTGTTGGGCATGATGCTGTTGCTTT	1306
Db	401	ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu	420
QY	1307	AATCCAATTCATATGGGTTTCTTAATAATGGGATTAAAGCTGATTTAGTGTCCCTTATA	1366
Db	421	AsnProIleLeuTyrGlyPheLeuAsnGlyIleLysAlaAspLeuValSerLeuIle	440
QY	1367	CACTGTCTTCATATG	1381
Db	441	HisCysLeuHisMet	445

Search completed: October 21, 2004, 12:01:22
 Job time : 65 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 21, 2004, 11:40:49 ; Search time 186 Seconds
(without alignments)

4894.673 Million cell updates/sec

Title: US-09-771-956-4

Perfect score: 2480

Sequence: 1 ttttggtgtgacaaatgt.....attctcactgtttaccaagg 1406

Scoring table: BLOSUM62

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Xgapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 2729282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_p/US09771956/runat_21102004_103739_9430/app_query.fasta_1.1543

-DB=published Applications AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1

-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=ptc -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=200000000 -USER=US09771956@cgn_1_1_211_@runat_21102004_103739_9430

-NCFU=6 -ICFU=3 -NO_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:

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19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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Alignment Scores:	3.11e-223	Length:	455
Pred. No.:	2385.00	Matches:	455

ALIGNMENTS

RESULT 1

US-09-771-956-13
; Sequence 13, Application US/09771956
; Patent No. US20010031474A1

; GENERAL INFORMATION:

; APPLICANT: Bennett, Michele

; APPLICANT: Brodbeck, Robbin

; APPLICANT: Krause, James

; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors

; FILE REFERENCE: N2000.001

; CURRENT APPLICATION NUMBER: US/09/771,956

; CURRENT FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 455

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-771-956-13

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 9 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-771-956-13 (1-455)

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 QY 77 AAGACACTGGCAGAGAAATAACTCTGCTCCACTCGGAATTTCTGATTTCCCAAGTCTGG 136
 DB 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
 QY 137 GATGACTATAAAGCAGTGTAGATGACTTACAGTATTTCTGATGGGCTCTATACATTT 196
 DB 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
 QY 197 GTAAGTCTTCTTGGCTTTATGGGAATCTACTTATTTTAAATGGCTCTCATGAAAAAGCGT 256
 DB 61 ValSerLeuLeuGlyPheValGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg 80
 QY 257 AATCAGAGACTACGGTAAACTCTCTCATAGCAATCTGGCCTTTCTGATATCTTGGTT 316
 DB 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
 QY 317 GTGCTGTTTCTGCTACCTTTCACACTGACCTCTGCTTGGTGGATCAGTGGATGTTGGC 376
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 QY 377 AAAGTCATGTGCGATATATGCTTTTCTTCAATGTGTGTCAGTATTTTGGTTTCAACTTTA 436
 DB 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 QY 437 ATTTTAATATCAATTCATGCTGTCAGTATCATATGATAAACAATCCCATATCTAAAT 496
 DB 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
 QY 497 TTAACAGCAAAACATGGCTACTTTCTGATAGTCTGCTGACACTAGGTTTGGCCATC 556
 DB 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle 180
 QY 557 TGTTCCTCCCTTCCAGTCTTTTACAGTCTTCTGGAATTCAGAAACATTTGGTTCAGCA 616
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 QY 617 TTGCTGACACAGCATTTATGTTGAGTCATGGCCATCTGATTCATACAGAAATGCC 676
 DB 201 LeuLeuSerSerArgTyrLeuCysValGluSerTyrProSerAspSerTyrArgIleAla 220
 QY 677 TTTACTATCTCTTTATCTAGTTTCAATATTTCTGCCCTTAGTTTGTCTTACTGTAGT 736
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 QY 737 CATACAAGTCTGCGAAGATTAAGCTGTGATGTGTCATGTCACAAAGAAACAGCTTGAA 796
 DB 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 QY 797 GAAATGAGATGATCAACTTAACCTTCTCATCCATCCAAAAGAGTGGGCTCAGTGCAAA 856
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 DB 281 LeuSerGlySerHisLysTyrSerTyrSerPheIleLysLysHisArgArgTyrSer 300
 QY 917 AAGAGACAGCATGTGCTTACCTGCTCCAGAAAGACCTTCTCAAGAAACCACTCCAGA 976
 DB 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
 QY 977 ATACTCCAGAAACATTTGGCTCTGTGAAGAGTCAGTCTCTTTCATCCAGTATGTTCA 1036

RESULT 2

US-09-962-646-4
 ; Sequence 4, Application US/09962646
 ; Patent No. US2002010123A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GERALD, CHRISTOPHE P.G.
 ; APPLICANT: WEINSHANK, RICHARD L.
 ; APPLICANT: WALKER, MARY W.
 ; APPLICANT: BRANCHEK, THERESA
 ; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
 ; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR
 ; FILE REFERENCE: 1795/46166BZA
 ; CURRENT APPLICATION NUMBER: US/09/962,646
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/200,673
 ; PRIOR FILING DATE: 1998-11-25
 ; PRIOR APPLICATION NUMBER: 08/566,096
 ; PRIOR FILING DATE: 1995-12-01
 ; PRIOR APPLICATION NUMBER: 08/349,025
 ; PRIOR FILING DATE: 1994-12-01
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 455
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-09-962-646-4

Alignment Scores:
 Pred. No.: 3,118-223 Length: 455
 Score: 2385.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 9 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-962-646-4 (1-455)

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 QY 77 AAGACACTGGCAGAGAAATAACTCTGCTCCACTCGGAATTTCTGATTTCCCAAGTCTGG 136
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 QY 137 GATGACTATAAAGCAGTGTAGATGACTTACAGTATTTTCTGATGGGCTCTATACATTT 196

Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuLeuGlyLeuTyrThrPhe 60
Qy 197 GTAAGTCTCTTGGCTTATGGGAAATCTATTATTTAATGCTCTCATGAAAGCGT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg 80
Qy 257 AATCAGAGACTACGGTAAACTCCATAGGAATCTGGCTTCTGTATCTGGTT 316
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Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
Qy 377 AAAGTCATGTGCCATATATGCTTTCTTCAATGCTGTGTCAGTGGTTTCAACTTAA 436
Db 121 LysValMetCysHisLeuMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
Qy 437 ATTTTAATATCAATGCGATGTCAGGTATCATATGATAAAACATCCCATATCTATAAT 496
Db 141 IleLeuLeuSerIleAlaIleValArgTyrHisMetIleLysHisProLieserAsnAsn 160
Qy 497 TTAACAGAAACCATGCTACTTTCTGATGCTACTCTCTGGACACTAGGTTTTGGCATC 556
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Qy 557 TGTCTCCCTTCCAGTGTTCACAGCTTGTGGAAGCTTCAAGAAACATTTGTTGAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
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Qy 677 TTTACTATCTTTTATGCTAGTTAGTCAGTATATCTGCTTGTGCTTCTTACTGAGT 736
Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
Qy 737 CATCAAGTGTCTGCAGAGTATAGCTGTGGATTGTCCAAAGAAAGAAACAGACTTGA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
Qy 797 GAAATGAGATGATCAACTTAACCTTTCATCCATCCAAAAGAGTGGGCTCAGGTGAAA 856
Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
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Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
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Qy 1337 GGGATTAAGCTGATTTAGTGTCCCTTATACACTGCTCTTCATATG 1381
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RESULT 3

US-10-013-846-7
; Sequence 7, Application US/10013846
; Publication No. US20030036652A1
; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Brielmann, Harry L
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Maryls
; TITLE OF INVENTION: Spiroisobenzofuran-1,4'-piperidin]-3-ones and
; FILE REFERENCE: NO.2001
; CURRENT APPLICATION NUMBER: US/10/013,846
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 455
; TYPES: PRT
; ORGANISM: homosapiens
US-10-013-846-7

Alignment Scores:
Pred. No.: 3,11e-223 Length: 455
Score: 2385.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 96.17% Indels: 0
DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-013-846-7 (1-455)

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 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle 180
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 Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
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 Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
 QY 737 CATACAGTGTCTGAGAGATTAAGCTGTGGATGTCCAAACAAAGAAACAGACTTGAA 796
 Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
 QY 797 GAAATGAGATGATCAACTTAACCTTCTCATCTCCAAAGAGTGGGCTCAGTGCAAA 856
 Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
 QY 857 CTCTCTGCGACCCATAAATGAGTATTCAATTCATCAAAAAACACAGAAAGATATAGC 916
 Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
 QY 917 AAGAGACAGCATGTGTTTACCTGCTCCAGAAAGCTTCTCAGAGAACCCACTCCAGA 976
 Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
 QY 977 ATACTTCCAGAAAATTTGGCTCTCTGAGAGAGTCAAGTCTCTTCCATCCAGTAAGTTCA 1036
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 QY 1037 CCAGGGTCCCACTTGTCTTGGATGATAAATCACTGAGAAATTCAGATGTCATGAATG 1096
 Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360
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 QY 1157 ACCATCTGATATATGATTTGCTGTTAGTTGGATGCCATACACCTTTTCCATGTGGTA 1216
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 QY 1337 CGGATTAAAGCTGATTTAGTCTCTTATACACTGCTCTTCATATG 1381
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RESULT 4
 US-10-410-648-7
 ; Sequence 7, Application US/10410648
 ; Publication No. US20040072847A1

; GENERAL INFORMATION:
 ; APPLICANT: Bakthavatchalam, Rajagopal
 ; APPLICANT: Blum, Charles A.
 ; APPLICANT: Brielmann, Harry L.
 ; APPLICANT: Darrow, James W.
 ; APPLICANT: De Lombaert, Stephanie W.
 ; APPLICANT: Hutchinson, Alan W.
 ; APPLICANT: Tran, Jennifer W.
 ; APPLICANT: Zheng, Xiaozhang W.
 ; APPLICANT: Elliott, Richard L.
 ; APPLICANT: Hammond, Marlys L.
 ; TITLE OF INVENTION: SPRI[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
 ; FILE REFERENCE: 3H-SPRI[ISOBENZOFURAN-1,4'-PIPERIDINES
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: 10/013,846
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: 60/254,990
 ; PRIOR FILING DATE: 2000-12-12
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 455
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-10-410-648-7

Alignment Scores:
 Pred. No.: 3,11e-223 Length: 455
 Score: 2385.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.17% Indels: 0
 DB: 15 Gaps: 0
 US-09-771-956-4 (1-1406) x US-10-410-648-7 (1-455)
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 Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
 QY 77 AAGACACTTCCACAGACAATAATCTGCTGCACTCGCAATTCCTGATTTCCCACTCTGG 136
 Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
 QY 137 GATGACTATAAAGCAGTGTAGATGACTACAGTATTTTCTGATTTGGGCTCTATACATT 196
 Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
 QY 197 GTAAGTCTTCTGGCTTTATGGGGAATCTACTATTTTAAATGGCTCTCATGAAAAAGCGT 256
 Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
 QY 257 ATACAGACACTACGGTAACTTCTCTCATAGCAATCTGGCTTTTCTGATATCTTGTT 316
 Db 81 AsnGlnLysThrThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
 QY 317 GTGCTGTTTGTCTCACTTCTCACTGACGCTGCTTCTGCTGGATCAGTGGATGTTTGGC 376
 Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpPheGly 120
 QY 377 AAGATCATGTGCCATATATGCTTTTCTCAATGTGTGTCAGTTTGGTTTCACTTTA 436
 Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
 QY 437 ATTTTAATATCAATTCGATTCAGTGTATCATATGATAAATCCCATATCTAATAAT 496
 Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
 QY 497 TTAACAGCAAAACCATGGCTACTTTCTGATAGTACTGTCTGACACTAGGTTTGGCCATC 556
 Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTyrThrLeuGlyPheAlaIle 180

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QY 557 TGTTCCTCCCTTCAGTGTGTTTCACAGTCTTGCGAATTCAGAAACATTTGGTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200
QY 617 TTGTCGACGACGAGTATTTATGTTGTTGAGTCTATGGCCATCTCATTCATACAGAAATGGC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY 677 TTTACTATCTCTTTATGCTAGTTCAGTATATCTGCGCTTGTGCTTGTCTTACTGTAAGT 736
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QY 737 CATCAAGTGTCTCCAGAGTATAAGCTGTGATTTGTCACAAAGAAAGAAACAGACTTGAA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
QY 797 GAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAAGAGTGGGCCCTCAGGTGAAA 856
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QY 857 CTCTCTGCAGCCATAAATGAGTTATTCATTCATCAAAAACACAGAGAAGATATAGC 916
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QY 1217 ACTGATTTTAAATGCAATCTTATTTCAATAGGCATTTCAAGTTGGTGTATTGCATTTGT 1276
Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY 1277 CATTTGTGGCATGATGCTCTGTGTTCTTAATCCAATTTCTATATGGGTTTCTTAATAT 1336
Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY 1337 GGGATTAAAGCTGATTTAGTGTCTTATACACTGTCTTCATATG 1381
Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 5
US-09-771-956-30
; Sequence 30, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brobeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 30
; LENGTH: 455

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; TYPE: PRT
; ORGANISM: Cercopithecus aethiops
US-09-771-956-30
Alignment Scores:
Pred. No.: 4,596-222 Length: 455
Score: 2373.00 Matches: 452
Percent Similarity: 99.78% Conservative: 2
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 95.69% Indels: 0
DB: 9 Gaps: 0

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US-09-771-956-4 (1-1406) x US-09-771-956-30 (1-455)

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QY 17 ATGTCTTTTATTTTCAAGCAGGACTATAATATGGATTTAGAGCTCGCAGATATTATAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
QY 77 AAGACACTTGGCCACAGAGAATAATCTGCTGCCATCTCGGAATCTGATTTCCCACTCTGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
QY 137 GATGACTATAAAGCAGTGTAGATCACTTACAGTATTTTCTGATTTGGGCTCTATACATT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAAGTCTTCTTGGCTTTATGGGAATCTACTTATTTTAAATCGCTCTCATGAAAAGCGT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
QY 257 ATCAGAGACTACGGTAAACTTCTCATAGCAATCTGGCCTTTTCTGATATCTTGTT 316
Db 81 AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY 317 GTGCTGTTTGTCTCACCTTTTCACTGACGCTGTCTGCTCGATCGAGTGGATGTTTGGC 376
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY 377 AAGTCATGTGCCATATATAGCTTTTCTTAAATGTGTGTGTCAGTTTGGTTTCACTTTA 436
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY 437 ATTTTAATATCAATGCGCTTGTAGGATCATATGATAAAACATCCCATATCTTAATAT 496
Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisIlePheSerAsnAsn 160
QY 497 TTAACAGCAAAACCATGGCTACTTTCGTATGACTGTCTGACACTAGGTTTGGCCATC 556
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
QY 557 TGTCTCTCCCTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTTGGTTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnThrPheGlySerAla 200
QY 617 TTGCTGAGCAGCAGGATATTTATGTTGAGTGTATGCGCATGCGCCATCTGATTCACAGAATTGCC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY 677 TTTACTATCTCTTTATGCTAGTTCAGTATATTCGCGCTTGTGCTTGTCTTACTGTAAGT 736
Db 221 PheThrIleSerLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
QY 737 CATCAAGTGTCTCCAGAGATATAAGCTGTGATTTGTCACAAAGAAAGAAACAGACTTGAA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
QY 797 GAAATGAGATGATCAACTTAACTCTTCATCCATCCAAAAGAGTGGGCCCTCAGGTGAAA 856
Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerArgLysIleGlyProGlnValLys 280
QY 857 CTCTCTGCAGCCATAAATGAGTATTTCATTCATCAAAAACACAGAGAAGATATAGC 916
Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300

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QY 917 AAGAGACAGCATGTGTTTACCTGCTCCAGAAAGACCTTCTCAAGAGACCACTCCAGA 976
Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
QY 977 ATACTTCCAGAAAACCTTTGGCTCTGTGAAGAAGTCAAGTCTCTTCCATCCAGTAAGTTCATA 1036
Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
QY 1037 CCAGGGTCCCACTTGGCTTTGAGATAAAACCTCAAGAAATTCAGATGTCATGAATTG 1096
Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360
QY 1097 AGAGTAAACGTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156
Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
QY 1157 ACCATACTGATATTAGTATTGCTGTAGTTGGATGGACACACACCTTTCCATGGTA 1216
Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY 1217 ACTGATTTTAAATGACAATCTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCAATTTG 1276
Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyrCysIleCys 420
QY 1277 CATTTGTTGGGCATGATGCTCTGTGTTCTTAATCCAATTCATATGGGTTTCTTAAATAAT 1336
Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
QY 1337 GGGATTAAGTCATTTAGTGTCCCTTATACACGTCTCTCATATG 1381
Db 441 GlyIleLysAlaAspLeuMetSerLeuIleHisCysLeuHisMet 455

RESULT 6
US-10-274-851-7
; Sequence 7, Application US/10274851
; Publication No. US20030144290A1
; GENERAL INFORMATION:
; APPLICANT: Blum, Charles
; APPLICANT: Brielmann, Harry
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Zheng, Xiaozhang
; TITLE OF INVENTION: SUBSTITUTE 2-CYCLOHEXYL-4-PHENYL-1H-IMIDAZOLE
; TITLE OF INVENTION: DERIVATIVES
; FILE REFERENCE: U 014209-8
; CURRENT APPLICATION NUMBER: US/10/274,851
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-851-7

Alignment Scores:
Pred. No.: 1,41e-221 Length: 455
Score: 2368.00 Matches: 453
Percent Similarity: 99.56% Conservative: 0
Best Local Similarity: 99.56% Mismatches: 2
Query Match: 95.48% Indels: 0
DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-274-851-7 (1-455)
QY 17 ATGCTTTTATTCACAGCAGCATATAATATGATTTAGCTCGCAGCATATTATAAC 76
Db 1 MetSerPheTyrSerLysGlnAspTyrAsnMetAspLeuGluLeuAspGluTyrTyrAsn 20
QY 77 AAGACACTTGCACAGAAATAACTGCTGCCACTCGGAATTCGATTTCCCACTGCG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTrp 40
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QY 137 GATGACTATAAAAGCAGTGTAGATGACTTACAGTATTTTCTGATTGGCTCTATACATTT 196
Db 41 AspAspTyrLysSerSerValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPhe 60
QY 197 GTAAGTCTTTGGCTTTTATGGGAATCTACTATTATTTAAATGGCTCTCATGAAAAGCGT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuIleLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAGAACACTACGTAACCTTCTCATAGGCAATCTGGCCCTTTCTTGATATCTTGTT 316
Db 81 AsnGlnLysThrValAsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY 317 GTGCTGTTTGTCTCACCTTTTCACACTGACGTCTGTCTTCTGGATCAGTGAATGTTGGC 376
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY 377 AAGATCATGTGCATATTATAGCTTTTCTTCAATGTGTCTAGTGTCTTGGTTTCACTTTA 436
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY 437 ATTTTAAATATCAATTGCCATTGTCAGGTATCATATGATAAAACATCCCATATCTAATAAT 496
Db 141 IleLeuIleSerIleAlaIleValArgTyrHisMetIleLysHisProIleSerAsnAsn 160
QY 497 TTAACAGCAACCATGGCTACTTTTCTGATAGCTACTGTCTGGACACTAGGTTTGGCCATC 556
Db 161 LeuThrAlaAsnHisGlyTyrPheLeuIleAlaThrValTrpThrLeuGlyPheAlaIle 180
QY 557 TGTCTCCCTTCCAGTGTTCACAGTCTTGTGGAACTTCAAGAAACATTTGGTTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
QY 617 TTGCTCAGCAGCAGTATTATTGCTTTCAGTCATGCGCATCTGTATCATACAGAAATGCC 676
Db 201 LeuLeuSerSerArgTyrLeuCysValGluSerTrpProSerAspSerTyrArgIleAla 220
QY 677 TTTACTATCTCTTTATTCAGTGTATATCTGCGCTTAGTGTCTTACTGTAGT 736
Db 221 PheThrIleSerLeuLeuLeuValGlnTyrIleLeuProLeuValCysLeuThrValSer 240
QY 737 CATACAAGTGTCTGCAGAAAGTATAAGCTGTGGATTGTCCAAACAAAGAAACAGACTTGAA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerTrpLysGluAsnArgLeuGlu 260
QY 797 GAAATGAGATCATCACTTAACCTTCTCATCCATCCAAAAGAGTGGCGCTCAGGTGAA 856
Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
QY 857 CTCTCTGGCAGCCATAAATGGAGTTATTTCATTTCATCAAAAACACAGAAAGATATAGC 916
Db 281 LeuSerGlySerHisLysTrpSerTyrSerPheIleLysLysHisArgArgTyrSer 300
QY 917 AAGAAGACAGCATGTGTGTTACTCTCCAGAAAGACCTTCTCAAGAAACACACTCCAGA 976
Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
QY 977 ATACTTCCAGAAAACCTTTGGCTCTGTAAGAAGTCAAGCTCTCTTCATCCAGTAAGTTTATA 1036
Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
QY 1037 CCAGGGTCCCACTTGGCTTTGAGATAAAACCTGAAGAAATTCAGATGTTTCATGAATTG 1096
Db 341 ProGlyValProThrCysPheGluIleLeuProGluGluAsnSerAspValHisGluLeu 360
QY 1097 AGAGTAAACGTTCTGTTTACAGAAATAAAAGAGATCTCGAAGTGTGTTTCTACAGACTG 1156
Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyrArgLeu 380
QY 1157 ACCATACTGATATTAGTATTGCTGTAGTTGGATGGCACTACACCTTTCCATGGTA 1216
Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY 1217 ACTGATTTTAAATGACAATCTATTTCAAATAGGCATTTCAAGTTGGTGTATTGCAATTTG 1276
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Db 401 ThrAspPheAsnAspAsnLeuLeuSerAsnArgHisPheLysLeuValTyrCysIleCys 420
 Qy 1277 CATTTGTTGGCAGTGTCTGTTGCTTAATCCAAATTTCTATATGGGTTTCTTAATAAT 1336
 Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyrGlyPheLeuAsnAsn 440
 Qy 1337 GGGATTAAAGCTGATTAGTGTCCCTTATACACTGCTTTCATATG 1381
 Db 441 GlyIleLysAlaAspLeuValSerLeuIleHisCysLeuHisMet 455

RESULT 7

US-10-027-049-6
 ; Sequence 6, Application US/10027049
 ; Publication No. US20030022283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu Ph.D., Yinghe
 ; McCalieb Ph.D., Michael L.
 ; Bloomquist Ph.D., Brian T.
 ; Flores-Riveros Ph.D., Jaime R.
 ; Cornfield Ph.D., Linda J.
 ; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
 ; Sequences
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive, 32nd Floor
 ; CITY: Chicago
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60606
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/027,049
 ; FILING DATE: 08-Apr-1996
 ; CLASSIFICATION: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Greenfield Ph.D., Michael S.
 ; REGISTRATION NUMBER: 37,142
 ; REFERENCE/DOCKET NUMBER: 96,149/MH 405
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 715-1000
 ; TELEFAX: (312) 715-1234
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 445 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-027-049-6
 Alignment Scores:
 Pred. No.: 7,03e-218 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-027-049-6 (1-445)

Qy 47 ATGGNTTTAGAGCTCGAGCTATATATACAGACACTTGCACAGAGATATACCTGCT 106
 Db 1 MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
 Qy 107 GCCACTCGGAATTTCTGATTTCCCACTCTGGAGTCACTATAAAGCAGTGTAGATGACTTA 166
 Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerSerValAspLeu 40

Qy 167 CAGTATTTCTGATTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTTATGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
 Qy 227 CTTATTTTAATGGCTCTCATGAAGAAGGTATCAGAGACTACCGTAACCTTCCTCAT 286
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuIle 80
 Qy 287 GGCATCTCTGGCCCTTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTTCACACTGAG 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
 Qy 347 TCTGCTCTCTGATCAGTGGATGCTTGGCAAGCACTATGTCATATATATGCTTTCTT 406
 Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu 120
 Qy 407 CAATGTGTCTCAGTCTTGGTCTTCAACTTTAAATATCAATTCACATTCAGGTAT 466
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140
 Qy 467 CATATGATAAAACATCCCATATCTAATATTTAAACAGCAAAACCATGGCTACTTTCTGATA 526
 Db 141 HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
 Qy 527 GCTACTGCTGGACACTAGTGTTCCTCTCTCCCTTCCAGTGTTCACAGTCTT 586
 Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
 Qy 587 GTGGAACCTTCAAGAAACATTTGTTTTCAGCANTGCTGACGACGAGTATTTATGTGTGAG 646
 Db 181 ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu 200
 Qy 647 TCATGGCCATCTGATTCATACAGAAATTCGCTTACTATCTCTTTTATGCTACTTCTAGTAT 706
 Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
 Qy 707 ATTCTGCCCTTAGTGTCTTACTGTAAGTCTACAAAGTGTCTGCAGAAGTATAAGCTGT 766
 Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
 Qy 767 GATTTGTCACAAAGAAACAGACTTGAAGAAATAGATGATCACTTACTCTTCTAT 826
 Db 241 GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis 260
 Qy 827 CCATCCAAAAAGAGTGGGCTCAGGTGAACCTCTCTGGCAGCCATAAATGGAGTATTCA 886
 Db 261 ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer 280
 Qy 887 TTCATCAAAAAACACAGAAAGATATAGCAAGAGACAGCATGTGTGTACTCTGCTCCA 946
 Db 281 PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
 Qy 947 GAAGACCTTCTCAAGAGAACCACTCCAGAACTTCCAGAAACCTTTGGCTCTGTAAGA 1006
 Db 301 GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg 320
 Qy 1007 AGTCAGCTCTCTTCATCCAGTAAGTTTCATACACAGGGGTCCCACTTGTCTTGGAGATAAAA 1066
 Db 321 SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys 340
 Qy 1067 CTTGAAGAAAAATTCAGATGTTTCATGAATTCAGAGTAAACCGTCTCTGTTACAGAAATAAA 1126
 Db 341 ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys 360
 Qy 1127 AAGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTATATTAGTATTGCTGTAGT 1186
 Db 361 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleValPheAlaValSer 380
 Qy 1187 TGGATCCCACTACACCTTTTCCATGTTGTTAACTGATTTTAAATGACAATCTTATTTCAAAT 1246
 Db 381 TrpMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 400

QY 1247 AGCAATTCAGATTGGTGGTATTGCAATTTGTCATTTCTGGGCATGATGCTCTGTGTGCTT 1300
 Db 401 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu 420
 QY 1307 AATCAATTCATATGCGTTTCTTAATAATGGGATTAAAGCTGATTAGTGTCCCTTATA 1366
 Db 421 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle 440
 QY 1367 CACTGCTTTCATATG 1381
 Db 441 HisCysLeuHisMet 445
 RESULT 8
 US-10-225-567A-205
 ; Sequence 205, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burmer, Joseph C.
 ; APPLICANT: Roush, Christene L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 205
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-225-567A-205
 Alignment Scores:
 Pred. No.: 7,03e-218 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 14 Gaps: 0
 US-09-771-956-4 (1-1406) x US-10-225-567A-205 (1-445)
 QY 47 ATGATTTAGACTCGACGAGTATTATACAGACACTTGGCCACAGAAATAACTGCT 106
 Db 1 MetAspLeuGluLeuAspGluTyrTyraAsnLysThrLeuAlaThrGluAsnAsnThrAla 20
 QY 107 GCACACTCGCAATTCGTATTCACAGCTCGGATGACTATAAAAGCAGTGTAGACTCTTA 166
 Db 21 AlaThrArgAsnSerAspPheProValTyrAspAspTyrLysSerSerValAspAspLeu 40
 QY 167 CAGTATTTTCGATTTGGCTCTATACATTTGTAAAGTCTTCTTGGCTTTATCGGGAATCTA 226
 Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMet-GlyAsnLeu 60
 QY 227 CTATTTTAAATGGCTCTCATGAAAAAGCGTAATACAGAACACTACGGTAAACTTCTCAT 286
 Db 61 LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuIle 80
 QY 287 GCCAATCTGGCCTTTTCTGATATCTTGGTTGTGCTCTTTTGTCTACCTTTGCACACTGACG 346
 Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
 QY 347 TCTGTCTTGTGCGATCAGTGGATGTTTGGCAAGTCATGTGCCATATTATGCTTTTCTT 406
 Db 101 SerValLeuLeuAspGlnTyrMetPheGlyLysValMetCysHisIleMet-ProPheLeu 120
 QY 407 CAATGTGTGCTGATTTGGTTTCTCACTTTAATTTTAATCAATTTGCCATTTGCTAGTAT 466
 Db 121 GlnCysValSerValLeuValSerThrLeuIleLeuIleSerIleAlaIleValArgTyr 140

467	QY	CATATGATAAACATCCCATATCTANTATATTTAACAGCAAAACATGGCTACTTCTCGATA	526
141	DB	HisMetIleGlyHisProIleSerAsnAsnLeuThrAlaAsnHisGlyIyrPheLeuIle	160
527	QY	GCTACTGTCGTGACACTAGGTGTTTTGCCATCTGTCTCCCTTCCAGTGTTCACAGCTCT	596
161	DB	AlaThrValIrrThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu	180
587	QY	GTGGAACTTCAAGAAACATTTGGTTCAGCATTCCTGACGACGAGAGTATTATTGTGTGAG	646
181	DB	ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgIyrLeuCysValGlu	200
647	QY	TCATGGCCACTCTGATTTCATACAGAAATGGCTTTACTATCTCTTTATTGTGTAGTTCAGTAT	706
201	DB	SerIrrProSerAspSerIyrArgIleAlaPheThrIleSerLeuLeuValGlnIyr	220
707	QY	ATTCTGCCCTTAGTTGTCTTACTGTAAGTCATACAAGTGTCTGCAGAGATGATAAGCTGT	766
221	DB	IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys	240
767	QY	GGATTCTCAACAAAGAAACACAGACTTGAAGAAAATGAGATGATCAACTAACTCTTCAT	826
241	DB	GlyLeuSerAsnIysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis	260
827	QY	CCATCCAAAAAGAGTGGGCTCAGGTGAACACTCTCTGGCAGCCATATAATGGAGTTATCCA	886
261	DB	ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysIrrSerIyrSer	280
887	QY	TTTCATCAAAAAACACAGAGAAGATATACAGAAGACAGCATGTCTGTTTACCTGCTCCA	946
281	DB	PheIleLysHisIrrgargIyrSerLysLysThrAlaCysValLeuProAlaPro	300
947	QY	GAAAGACCTTCTCAAGAGAACCACTCCAGAATACTTCCAGAAAACTTGGCTGTGTAGA	1006
301	DB	GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg	320
1007	QY	AGTCAGCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACATGGCTTTCAGAGATAAA	1066
321	DB	SerGlnLeuSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys	340
1067	QY	CCTGAAGAAAAATTCAGATGTTTCATGAATTCAGAGTAAAAACGTTCTCTTCAAGAATAAAA	1126
341	DB	ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys	360
1127	QY	AGAGATCTCGAAGTGTTTTTTCACAGACTGCACACTACTGATATTAGTATTGCTGTACT	1186
361	DB	LysArgSerArgSerValPheIyrArgLeuThrIleLeuIleLeuValPheAlaValSer	380
1187	QY	TGGATGCCACTACACCTTTTCATCTGGTGAATGATTTTAAATGCACAACTCTTATTTCAAAT	1246
381	DB	TrrMetProLeuHisLeuPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn	400
1247	QY	AGGCATTCGAAGTGTGTATTGTCATTTGTCATTGCTGGGCAATGATGCTCTGTGTCTTT	1306
401	DB	ArgHisPheLysLeuValIyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu	420
1307	QY	ATTCCAAATTCATATGGGTTTCTTAATAATGGATTAAGCTGATTTAGTGTCCCTTATA	1366
421	DB	AsnProIleLeuIyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle	440
1367	QY	CAGTGTCTTCATATG	1381
441	DB	HisCysLeuHisMet	445

APPLICANT: Glynn, Richard
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-01250005
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 668
 LENGTH: 445
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-668

Alignment Scores:
 Pred. No.: 7,03e-218 Length: 445
 Score: 2330.00 Matches: 445
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.95% Indels: 0
 DB: 14 Gaps: 0

US-09-771-956-4 (1-1406) x US-10-295-027-668 (1-445)

Qy	47	ATGGATTAGAGCTCGAGCTATTATACAGACACTTCCACAGAGATAATACTGCT	106
Db	1	MetAspLeuGluLeuAspGluTyrAsnLysThrLeuAlaThrGluAsnThrAla	20
Qy	107	GCCACTCGGANTCTGATTTCCAGTCTGGAGTACTATAAAGCAGTGTAGATGCTTA	166
Db	21	AlaThrArgAsnSerAspPheProValTrpAspAspTyrLysSerValAspAspLeu	40
Qy	167	CAGTATTTCGATTGGCTCTATACATTTGTAAGTCTTCTGGCTTTATGGGGAATCTA	226
Db	41	GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu	60
Qy	227	CTTATTATTAGGCTCTCATGAAAGCGTAAATCAGAGACTACGGTAAACTTCTCTATA	286
Db	61	LeuIleLeuMetAlaLeuMetLysLysArgAsnGlnLysThrValAsnPheLeuIle	80
Qy	287	GGCAATCTGGCTTTCTGATATCTTGTTGCTGCTGTTGCTCACCCTTTCCACTGACG	346
Db	81	GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr	100
Qy	347	TCTGCTCTGCTGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	406
Db	101	SerValLeuLeuAspGlnTrpMetPheGlyLysValMetCysHisIleMetProPheLeu	120

Qy	407	CAATGTGTGTCAGTTTGGTTTCACTTAAATTTAAATATCAATTCATTCAGGTAT	466
Db	121	GlnCysValSerValLeuValSerThrLeuLeuIleSerIleAlaIleValArgTyr	140
Qy	467	CATATGATAAACAATCCCATATCTAATAATTAACAGCAAAACCATGGCTACTTTCTGATA	526
Db	141	HisMetIleLysHisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle	160
Qy	527	GCTACTGTCTGACACTAGGTTTCCCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT	586
Db	161	AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu	180
Qy	587	GTGGAACCTTCAAGAAACATTTGGTTTCACTTGTGAGCAGCAGGTATTTATGTCTGAG	646
Db	181	ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu	200
Qy	647	TCATGCCCATCTGATTCATACAGAAATGCTTTACTATCTCTTTTCTGCTAGTTCAGTAT	706
Db	201	SerTyrProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuValGlnTyr	220
Qy	707	ATCTGCTCTTGTGTTTCTTACTTCTAGTCTATCAAGTGTCTGAGAGTATAAGTGT	766
Db	221	IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys	240
Qy	767	GGATTGTCCACAAAGAAACACAGACTTGAAGAAATGAGATGATCAACTTAACTTCTCAT	826
Db	241	GlyLeuSerAsnLysGluAsnArgLeuGluGluAsnGluMetIleAsnLeuThrLeuHis	260
Qy	827	CCATCAAAAGAGTGGGCTCAGTGAACTCTCTGCGAGCCATAAATGGAGTATTCACA	886
Db	261	ProSerLysLysSerGlyProGlnValLysLeuSerGlySerHisLysTrpSerTyrSer	280
Qy	887	TTTCATCAAAACACAGAGAGATATACAGAAAGATGAGATGATCAACTTAACTTCTCAT	946
Db	281	PheIleLysLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro	300
Qy	947	GAAAGACCTTCTCAAGAGAACCTCCAGATATCTCCAGAAACTTTGGCTCTGTAGA	1006
Db	301	GluArgProSerGlnGluAsnHisSerArgIleLeuProGluAsnPheGlySerValArg	320
Qy	1007	AGTCAGCTCTTCTCATCCAGTAAGTTCATACAGGGGTCCTCCACTTCTTTCAGATAAAA	1066
Db	321	SerGlnLeuSerSerSerSerLysPheIleProGlyValProThrCysPheGluIleLys	340
Qy	1067	CCTGAAGAAATTCAGATGTTTCATGAATTGAGATAAAGCGTTCGTGTTCACAGATAAAA	1126
Db	341	ProGluGluAsnSerAspValHisGluLeuArgValLysArgSerValThrArgIleLys	360
Qy	1127	AGAGATCTCGAAGTGTCTTCTACAGACTGACCATCTGATATTAGTATTGCTGTAGT	1186
Db	361	LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer	380
Qy	1187	TGATGCCACTACACCTTTTCCATGTGTAAGTATTTAATGACAATCTTATTTCAAT	1246
Db	381	TrpMetProLeuHisLeuPheHisValValValThrAspPheAsnAspAsnLeuIleSerAsn	400
Qy	1247	AGCATTTCAAGTGTGTGATTTGCATTTGTCATTTGTTGGGATCATGTCCTGTGTCTT	1306
Db	401	ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysCysLeu	420
Qy	1307	AATCCAAATCTATATGGGTTTCTTAAATATGGATTAAAGCTGATTAGTGTCCCTTATA	1366
Db	421	AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuValSerLeuIle	440
Qy	1367	CACTGTCTTTCATATG 1381	
Db	441	HisCysLeuHisMet 445	

RESULT 10
 US-10-181-906-14
 ; Sequence 14, Application US/10181906
 ; Publication No. US20040053864A1

GENERAL INFORMATION:			
APPLICANT: Karsenty, Gerard			
APPLICANT: Amling, Michael			
APPLICANT: Duvy, Patricia			
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA			
TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY			
FILE REFERENCE: 9142-020-999			
CURRENT APPLICATION NUMBER: US/10/181.906			
CURRENT FILING DATE: 2002-11-13			
PRIOR APPLICATION NUMBER: PCT/US01/02040			
PRIOR FILING DATE: 2001-01-22			
NUMBER OF SEQ ID NOS: 16			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 14			
LENGTH: 445			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-181-906-14			
Alignment Scores:			
Pred. No.:	7.03e-218	Length:	445
Score:	2330.00	Matches:	445
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	93.95%	Indels:	0
DB:	15	Gaps:	0
US-09-771-956-4 (1-1406) x US-10-181-906-14 (1-445)			
QY	47	ATGGATTAGAGCTCGACAGTATTATAACAGACACTTGCACAGAGATAATACTGCT	106
DB	1	MetAspLeuGluLeuAspGluTyrTyrAsnLysThrLeuAlaThrGluAsnThrAla	20
QY	107	CCACTCGGAATTCGATTTCCAGTCTGGGATCGACTATAAAGCAGTGTAGACTTA	166
DB	21	AlaThrArgAsnSerAspPheProValTyrAspAspTyrLysSerSerValAspLeu	40
QY	167	CAGTATTTCTGATTGGGCTCTATACATTTCTAGTCTTCTTGGCTTTATGGGAATCTA	226
DB	41	GlnTyrPheLeuLeuGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu	60
QY	227	CTTATTTAATGGCTCTCATGAAAGCGTAATCAGAGACTACGGTAAACTTCTCTATA	286
DB	61	LeuLeuLeuMetAlaLeuMetLysLysArgAsnGlnLysThrThrValAsnPheLeuLe	80
QY	287	GGCACTCGGCTTTCTGATATCTTGGTGTGCTGTTTGTCTCACCTTTACACTGACG	346
DB	81	GlyAsnLeuAlaPheSerAspLeuLeuValValLeuPheCysSerProPheThrLeuThr	100
QY	347	TCTGTCTTGGTGGATCGATGGATGTTTGGCAAGTCATGTGCCATATTATGCCCTTTCTT	406
DB	101	SerValLeuLeuAspGlnTyrMetPheGlyLysValMetCysHisLeuMetProPheLeu	120
QY	407	CAATGTGTGTCAGTTTGGTTTCACTTTATTTATTTATATCAATGCCATGTGAGTAT	466
DB	121	GlnCysValSerValLeuValSerThrLeuLeuLeuLeuSerLeuAlaLeuValArgTyr	140
QY	467	CATATGATAAAACATCCCATATCTAAATAATTTAAACAGCAACCATGCTACTTTCTGATA	526
DB	141	HisMetLysHisProLeuSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuLeu	160
QY	527	GCTACTGTCTGGACACTAGTTTGGCATCTGTTCTCCCTTCCAGTGTTCACAGTCTT	586
DB	161	AlaThrValTyrThrLeuGlyPheAlaLeuLeuCysSerProLeuProValPheHisSerLeu	180
QY	587	GTGGAACCTCAAGAAACATTTGGTTTGCAGCATTTGTGAGCAGCAGCATTTATGTGTGAG	646
DB	181	ValGluLeuGlnGluThrPheGlySerAlaLeuLeuSerSerArgTyrLeuCysValGlu	200
QY	647	TCATGGCCATCTGATTCATACAGAAATTCCTTTACTATCTCTTTATTCGTAGTTTCAGTAT	706
DB	201	SerTyrProSerAspSerTyrArgLeuAlaPheThrLeuSerLeuLeuValGlnTyr	220
US-09-771-956-9			
RESULT 11			
US-09-771-956-9			
Sequence 9, Application US/09771956			
Patent No. US20010031474A1			
GENERAL INFORMATION:			
APPLICANT: Bennett, Michele			
APPLICANT: Brobeck, Robbin			
APPLICANT: Krause, James			
TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors			
FILE REFERENCE: N2000.001			
CURRENT APPLICATION NUMBER: US/09/771.956			
CURRENT FILING DATE: 2001-01-29			
NUMBER OF SEQ ID NOS: 31			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 9			
LENGTH: 499			
TYPE: PRT			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: Y5/Y1 CHIMERA			
US-09-771-956-9			
Alignment Scores:			
Pred. No.:	1.77e-217	Length:	499
Score:	2326.00	Matches:	444

Percent Similarity: 99.78% Conservative: 1
Best Local Similarity: 99.55% Mismatches: 1
Query Match: 93.79% Indels: 0
DB: 9 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-771-956-9 (1-499)

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QY 17 ATGCTTTTATTCAGACAGACTATAATATGATTTAGAGCTCGACGAGTATTATAAC 76
Db 1 MetSerPheTySerLysGlnAspTyAsnMetAspLeuGluLeuAspGluTyTyAsn 20
QY 77 AAGACACTTGGCCAGACAGAAATAACTGCTGCCACTCGGAATTCCTGATTTCCCAAGTCTGG 136
Db 21 LysThrLeuAlaThrGluAsnAsnThrAlaAlaThrArgAsnSerAspPheProValTyr 40
QY 137 GATGACTATAAAGCAGTGTAGACTTACAGATATTTTCGATTTGGGCTCTATACATTT 196
Db 41 AspAspTyLysSerSerValAspAspLeuGlnTyPheLeuLeuLeuTyThrPhe 60
QY 197 GTAAGTCTTCTGCTTTATGGGAATCTACTATTTTAAATGGCTCTCATGAAAGACGCT 256
Db 61 ValSerLeuLeuGlyPheMetGlyAsnLeuLeuLeuMetAlaLeuMetLysLysArg 80
QY 257 AATCAGAGACTACGGTAAACTTCTCATAGGCAATCTGGCTTTTCTGATATCTTGTT 316
Db 81 AsnGlnTyThrThrValAsnPheLeuLeuLeuGlyAsnLeuAlaPheSerAspIleLeuVal 100
QY 317 GTGCTGTTTCTCACCTTTCACACTGACGCTGCTTGTGTCGATCAGTCGAGTGTGGC 376
Db 101 ValLeuPheCysSerProPheThrLeuThrSerValLeuLeuAspGlnTrpMetPheGly 120
QY 377 AAAGTCATGTGCCATATTATGCTTTTCTCAATGTGTGTCAGTGTGTTCACATTTA 436
Db 121 LysValMetCysHisIleMetProPheLeuGlnCysValSerValLeuValSerThrLeu 140
QY 437 ATTTTATATCAATGCCATTTGTCAGGTATCATATGATATAAACAATCCCATATCAATAAT 496
Db 141 IleLeuIleSerIleAlaIleValArgTyHisMetIleLysHisProIleSerAsnAsn 160
QY 497 TTAACAGCAACCACTGCTACTTTCTGATAGCTACTGTCGACACTAGGTTTTCGCATC 556
Db 161 LeuThrAlaAsnHisGlyTyPheLeuIleAlaThrValThrLeuGlyPheAlaIle 180
QY 557 TGTCTCCCTTCCAGTCTTTTACAGTCTTCTGGAACCTTCAAGAAACATTTGGTTCAGCA 616
Db 181 CysSerProLeuProValPheHisSerLeuValGluLeuGlnGluThrPheGlySerAla 200
QY 617 TTGTCAGCAGCAGGATTTATGCTTTCAGTCATGCGCATCTGATTCATACAGATTCGC 676
Db 201 LeuLeuSerSerArgTyLeuCysValGluSerTrpProSerAspSerTyArgIleAla 220
QY 677 TTTACTATCTCTTTATTCAGTATATTCTGCCCTTAGTCTTGTCTTACTGTAAGT 736
Db 221 PheThrIleSerLeuLeuValGlnTyIleLeuProLeuValCysLeuThrValSer 240
QY 737 CATCAAGTCTGAGAGATATAAGCTGTGGATTTCCCAACAAGAAACAGACTTGAA 796
Db 241 HisThrSerValCysArgSerIleSerCysGlyLeuSerAsnLysGluAsnArgLeuGlu 260
QY 797 GAAATGAGATGATCAACTTAACCTTTCATCCATCCAAAGAGTGGGCTTCAGGTGAAA 856
Db 261 GluAsnGluMetIleAsnLeuThrLeuHisProSerLysLysSerGlyProGlnValLys 280
QY 857 CTCTCGCAGCCATPAATAGGAGTTATTCATCATCAAAAAACAGAAAGATATAGC 916
Db 281 LeuSerGlySerHisLysTrpSerTySerPheIleLysLysHisArgArgTySer 300
QY 917 AAGAGACAGCATGTGCTTACCTCTCCAGAAAGACCTTCTCAAGAAACCTCCAGA 976
Db 301 LysLysThrAlaCysValLeuProAlaProGluArgProSerGlnGluAsnHisSerArg 320
QY 977 ATACTTCCAGAAAACCTTGGCTCTGTAAGAGAGTCAGCTCTCTTCTCATCAGTAAGTTCATA 1036
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Db 321 IleLeuProGluAsnPheGlySerValArgSerGlnLeuSerSerSerLysPheIle 340
QY 1037 CCAGGGTCCCACCTTGTCTTTCAGATAAAACCTGAAGAAAATTCAGATTTTCATGAATG 1096
Db 341 ProGlyValProThrCysPheGluIleLysProGluGluAsnSerAspValHisGluLeu 360
QY 1097 AGAGTAAACGTTCTGTTACAAGATATAAAAGAGATCTCGAAGTGTCTTCTACAGACTG 1156
Db 361 ArgValLysArgSerValThrArgIleLysLysArgSerArgSerValPheTyArgLeu 380
QY 1157 ACCATATCTGATATTAGTATTTCCTGTTAGTTCGATGCCACTACACTTTTCCATGTGGTA 1216
Db 381 ThrIleLeuIleLeuValPheAlaValSerTrpMetProLeuHisLeuPheHisValVal 400
QY 1217 ACTGATTTAAATGACAACTTCTTCAATAGGCAATTTCAAGTGTGTGATTGCAATTTCT 1276
Db 401 ThrAspPheAsnAspAsnLeuIleSerAsnArgHisPheLysLeuValTyCysIleCys 420
QY 1277 CATTTCTTGGCATGATGTCTGTTGCTTAAATCCAAATTCATATGGGTTTCTTAATAAT 1336
Db 421 HisLeuLeuGlyMetMetSerCysCysLeuAsnProIleLeuTyGlyPheLeuAsnAsn 440
QY 1337 GGGATTAAAGCTGATTTTA 1354
Db 441 GlyIleGlnArgAspLeu 446
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RESULT 12

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US-09-826-509-533
; Sequence 533, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 533
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-533
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Alignment Scores:
Pred. No.: 5,29e-217 Length: 445
Score: 2321.00 Matches: 444
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 93.59% Indels: 0
DB: 10 Gaps: 0

US-09-771-956-4 (1-1406) x US-09-826-509-533 (1-445)

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QY 47 ATGATTTAGAGCTCGACGAGTATTATAACAACACACTTCGCCACAGAGATATACTGCT 106
Db 1 MetAspLeuGluLeuAspGluTyTyAsnLysThrLeuAlaThrGluAsnThrAla 20
QY 107 GCCACTCGGAATTTCTGATTTCCCAAGTCTGGGATGACTATAAAAGCAGTGTAGATGACTTA 166
Db 21 AlaThrArgAsnSerAspPheProValTrpAspAspTyLysSerSerValAspLeu 40
QY 167 CAGTATTTCTGATTTGGGCTCTATACATTTGTAGTCTTCTTGGCTTTATGGGATCTTA 226
Db 41 GlnTyPheLeuIleGlyLeuTyThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
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Db      421 AsnProIleLeuTyrGlyPheLeuAsnGlyIleLysAlaAspLeuValSerLeuIle 440
Qy      1367 CACTGCTCTTCATATG 1381
Db      441 HisCysLeuHisMet 445

RESULT 13
US-09-962-646-2
; Sequence 2, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION:
; APPLICANT: GERALD, CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHEK, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR
; FILE REFERENCE: 1795/46166BZA
; CURRENT APPLICATION NUMBER: US/09/962,646
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/200,673
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566,096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349,025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Rattus No. US20020103123A1vegicus
US-09-962-646-2

Alignment Scores:
Pred. No.: 5,73e-194 Length: 456
Score: 2084.50 Matches: 396
Percent Similarity: 93.10% Conservative: 22
Best Local Similarity: 88.20% Mismatches: 30
Query Match: 84.05% Indels: 1
DB: Gaps: 1

US-09-771-956-4 (1-1406) x US-09-962-646-2 (1-456)
Qy      35 CAGGACTATAATGGATTGAGCTGCACGAGTATTATAACAAGACACTTGGCCACAGAG 94
Db      8 GlnAspSerSerMetGluPheLysLeuGluHisPheAsnLysThrPheValThrGlu 27
Qy      95 ANATAACTGCTGCACCTCGGAATCTCTGATTTCCAGCTCTGGGATGATATAAAGCAGT 154
Db      28 AsnAsnThrAlaAlaAlaArgAsnAlaAlaPheProAlaIleGluAspTyrArgGlySer 47
Qy      155 GTAGATGACTTACAGTATTTCTGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGCTTT 214
Db      48 ValAspAspLeuGlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPhe 67
Qy      215 ATGGGGAATCTACTTATTATTTAATGCTCTCATGAAAAAGCGTAAATCAGAAGACTACGGTA 274
Db      68 MetGlyAsnLeuLeuIleLeuMetAlaValMetLysLysLysArgAsnGlnLysThrThrVal 87
Qy      275 AACTTCCTCATAGGAATCTGCCCTTTTCTGATATCTTGGTTGTGCTGCTGTTTGTGCACCT 334
Db      88 AsnPheLeuIleGlyAsnLeuAlaPheSerAspIleLeuValLeuPheCysSerPro 107
Qy      335 TTCACACTGACCTCTGCTCTTGTGTCAGTCAGTGGATGTTTGGCAAGTCAATGTCATATT 394
Db      108 PheThrLeuThrSerValLeuLeuAspGlnTyrMetPheGlyLysAlaMetCysHisIle 127
Qy      395 ATGCCTTTTCTCAATGTGTGTACGCTTTTGTGTTTCACTTTAATTTAATATCAATTGCC 454
Db      128 MetProPheLeuGlnCysValSerValLeuValSerThrLeuIleLeuSerIleAla 147

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GENERAL INFORMATION:
APPLICANT: Hu Ph.D., Yinghe
McCaleb Ph.D., Michael L.
Bloomquist Ph.D., Brian T.
Flores-Riveros Ph.D., Jaime R.

[illegible]

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QY 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAAAACCATGGCTACTTCTGATA 526
Db 141 HisMetIleLeuHisProIleSerAsnAsnLeuThrAlaAsnHisGlyThrPheLeuIle 160
QY 527 GCTACTGTCTGACACTAGGTTTCCCATCTGTTCTCCCTCCAGTGTTCACAGCTTT 586
Db 161 AlaThrValThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
QY 587 GTGGAACTTCAAGAACATTTGGTTCAGCATTTGTCAGCAGCAGGTATTTATGTTGAG 646
Db 181 ValGluLeuLeuGluThrPheGlySerAlaLeuLeuSerSerLeuValGlu 200
QY 647 TCATGCCCATCTGATTTCATACAGAAATTCGCTTACTCTCTTTATTTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerThrArgIleAlaPheThrIleSerLeuLeuValGlnTyr 220
QY 707 ATTCTGCCCTTACTTGTCTACTGTAAGTATACAGTGTCTGCAGAGTATAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
QY 767 GGATTGTCCAAAGAAACAGACTTCAAGAAATGAGATGATCAACTTAACCTTTCAT 826
Db 241 GlyLeuSerHisGlyLeuAsnArgLeuGluAsnGluMetIleAsnLeuThrLeuGln 260
QY 827 CCATCAAAAGAGTGGGCCTCAGTGAACTCTCTGGCAGCCATAAATGAGTATATCA 886
Db 261 ProSerLysLysSerArgAsnGlnAlaLysThrProSerThrGlnLysTrpSerTyrSer 280
QY 887 TTCATCAAAAGAGTGGGCCTCAGTGAACTCTCTGGCAGCCATAAATGAGTATATCA 946
Db 281 PheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProIlePro 300
QY 947 GAAGACCTTCTCAAGAACCACTTCCAGATATCTTCCAGAAACTTTGGCTCTGTAGA 1006
Db 301 AlaGlyProSerGlnGlyLysHisLeuAlaVal--ProGluAsnProAlaSerValArg 319
QY 1007 AGTCAGCTCTTCTCATCAGTAAGTTTCATACAGGGTCCCTCCCTTGTGATATAAA 1066
Db 320 SerGlnLeuSerProSerSerLysValIleProGlyValProIleCysPheGluValLys 339
QY 1067 CTTGAAGAAATTCAGATGTTTCATGATTTGAGAGTAAACCTTCTGTGTACAGAAATAAA 1126
Db 340 ProGluGluSerSerAspAlaHisGluMetArgValLysArgSerIleThrArgIleLys 359
QY 1127 AAGAGATCTGAGTGTCTTCTACAGACTGACCATGATGATATAGTATTTGCTGTAGT 1186
Db 360 LysArgSerArgSerValPheThrArgLeuThrIleLeuIleValPheAlaValSer 379
QY 1187 TGGATGCCACTACACTTTTCCATGTGTAACTGATTTTATGATCAATCTTATTTCAAA 1246
Db 380 TrpMetProLeuHisValPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 399
QY 1247 AGGCAATTCAGTGTGTATGCAATTTGCTATTTGTTGGCATGATGCTGTGTCTT 1306
Db 400 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 419
QY 1307 AATCAATCTATATGGGTTTCTTAATAATGGGATTAAGCTGATTTAGTCTCCCTATA 1366
Db 420 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeuIle 439
QY 1367 CACTGTCTTCATATG 1381
Db 440 HisCysLeuHisMet 444

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RESULT 15

US-10-027-049-2

; Sequence 2, Application US/10027049

; Publication No. US2003002283A1

; GENERAL INFORMATION:

; APPLICANT: Hu Ph.D., Yinghe

; McCaleb Ph.D., Michael L.

; Bloomquist Ph.D., Brian T.

; Flores-Riveros Ph.D., Jaime R.
; Cornfield Ph.D., Linda J.
; TITLE OF INVENTION: Neuropeptide Y Receptor and Nucleic Acid
; Sequences

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff

; STREET: 300 South Wacker Drive, 32nd Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/10/027,049

; FILING DATE: 08-Apr-1996

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Greenfield Ph.D., Michael S.

; REGISTRATION NUMBER: 37,142

; REFERENCE/DOCKET NUMBER: 96,149/WH 405

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312)715-1000

; TELEFAX: (312)715-1234

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 445 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-027-049-2

Alignment Scores:

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Pred. No.: 2,588-192 Length: 445
Score: 2067.50 Matches: 393
Percent Similarity: 93.03% Conservative: 21
Best Local Similarity: 88.31% Mismatches: 30
Query Match: 83.37% Indels: 1
DB: 14 Gaps: 1

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US-09-771-956-4 (1-1406) X US-10-027-049-2 (1-445)

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QY 47 ATGGATTAGACTCGACGAGTATTATACAGACACTTGCACAGAGAAATAACTGCT 106
Db 1 MetGluPheLysLeuGluHisPheAsnLysThrPheValThrGluAsnThrAla 20
QY 107 GCACCTCGGAATTCGATTCCCGAGTCTGAGTAAAGCAGTGTAGATCACTTA 166
Db 21 AlaAlaArgAsnAlaPheProAlaIlePheGluAspTyrArgGlySerValAspLeu 40
QY 167 CAGTATTTCTGATTTGGGCTCTATACATTTGTAAGTCTTCTTGGGGAATCTA 226
Db 41 GlnTyrPheLeuIleGlyLeuTyrThrPheValSerLeuLeuGlyPheMetGlyAsnLeu 60
QY 227 CTTATTTTAAAGTCTCATGAAAGGCTATCAGACAGTACGTAAGTCTCTATA 286
Db 61 ProfileLeuMetAlaValMetLysLysArgAsnGlnLysThrValAspPheLeuIle 80
QY 287 GGCAATCTGGCCTTTTCTCATATCTTGTGTGTGCTGTTTGTCTACCTTTTCCACTGACG 346
Db 81 GlyAsnLeuAlaPheSerAspIleLeuValValLeuPheCysSerProPheThrLeuThr 100
QY 347 TCTGCTCTGCTGAGTACAGTGGATGTTTGGCAAGTCATGTGCATATATGCTTTTCTT 406
Db 101 SerValLeuLeuAspGlnTrpMetPheGlyLysAlaMetCysHisIleMetProPheLeu 120
QY 407 CAATGTGTCTCAGTTTGTGTTTCAACTTTAATTTAATATCAATTCGCAATTCAGGTAT 466

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Db 121 GlnCysValSerValLeuValSerThrLeuLeuLeuSerIleAlaIleValArgTyr 140
Qy 467 CATATGATAAAACATCCCATATCTAATAATTAAACAGCAAAACCATGGCTACTTTCTGATA 526
Db 141 HisMetIleIleYshisProIleSerAsnAsnLeuThrAlaAsnHisGlyTyrPheLeuIle 160
Qy 527 GCTACTGCTGGACACATAGGTTTGGCCATCTGTTCTCCCTTCCAGTGTTCACAGTCIT 586
Db 161 AlaThrValTrpThrLeuGlyPheAlaIleCysSerProLeuProValPheHisSerLeu 180
Qy 587 GTGGAACCTCAAGAAACATTTGGTTTCAGCATTTGTCAGCAGCAGGATTTATGTGTGTGAG 646
Db 181 ValGluLeuYshisGluThrPheGlySerAlaLeuLeuSerSerIleYshisLeuCysValGlu 200
Qy 647 TCATGGCATTCTGATTTCATACAGAAATGGCTTTACTATCTCTTTATTGCTAGTTCAGTAT 706
Db 201 SerTrpProSerAspSerTyrArgIleAlaPheThrIleSerLeuLeuLeuValGlnTyr 220
Qy 707 ATTCGTCCCTTAGTTTCTTACTTACTTAAGTCATACAAAGTGTCTGCAGAACTATAAGCTGT 766
Db 221 IleLeuProLeuValCysLeuThrValSerHisThrSerValCysArgSerIleSerCys 240
Qy 767 GGATTGTCCAAACAGAAACAGACTTCAAGAAATGAGATGATCAACTTAACCTTTTCAT 826
Db 241 GlyLeuSerHisLysGluAsnArgLeuGluAsnGluMetIleAsnLeuThrLeuGln 260
Qy 827 CCATCCAAAAGAGTGGCCCTCAGTGAACCTCTCTGGCAGCCATAAATGGAGTTATTCA 886
Db 261 ProSerLysLysSerArgAsnGlnAlaLysThrProSerThrGlnLysTrpSerTyrSer 280
Qy 887 TTCAATCAAAAACAGCAAGAGATATAGCAAGAGAGCAGCATGTGTGTACCTGTCTCCA 946
Db 281 PheIleArgLysHisArgArgTyrSerLysLysThrAlaCysValLeuProAlaPro 300
Qy 947 GAAAGACCTTCTCAAGAGAACCATCCAGATACTCCAGAAATCTTGGCTCTGTGAAGA 1006
Db 301 AlaGlyProSerGlnGlyLysHisLeuAlaVal---ProGluAsnProAlaSerValArg 319
Qy 1007 AGTCAGTCTCTTCATCCAGTAAGTTCATACAGGGGTCCCACTTCTGCTTTGAGATAAAA 1066
Db 320 SerGlnLeuSerProSerSerLysValIleProGlyValProlleCysPheGluValLys 339
Qy 1067 CCTGAAGAAATTCAGATGTTTCATCAATTGAGAGTAAACGTTCTGTTACAAGAAATAAA 1126
Db 340 ProGluGluSerSerAspAlaHisGluMetArgValLysArgSerIleThrArgIleLys 359
Qy 1127 AAGAGATCTCGAAGTGTCTTACAGACTGACCATGATGATATTAGTATTGCTGTAGT 1186
Db 360 LysArgSerArgSerValPheTyrArgLeuThrIleLeuIleLeuValPheAlaValSer 379
Qy 1187 TGGATGCCATACACCTTTTCCATGTGTGTAACATTTTAATGACAATCTTATTTCAAAT 1246
Db 380 TrpMetProLeuHisValPheHisValValThrAspPheAsnAspAsnLeuIleSerAsn 399
Qy 1247 AGGCATTTCAAGTTGGTGTATTGCAATTTGTCATTTGTTGGCATGATGCTGTTGCTT 1306
Db 400 ArgHisPheLysLeuValTyrCysIleCysHisLeuLeuGlyMetMetSerCysLeu 419
Qy 1307 AATCCAAATTCATATGGGTTTCTTAATAATGGGATTAAGCTGATTAGTGTCCCTTATA 1366
Db 420 AsnProIleLeuTyrGlyPheLeuAsnAsnGlyIleLysAlaAspLeuArgAlaLeuIle 439
Qy 1367 CACTGTCTTCATATG 1381
Db 440 HisCysLeuHisMet 444

